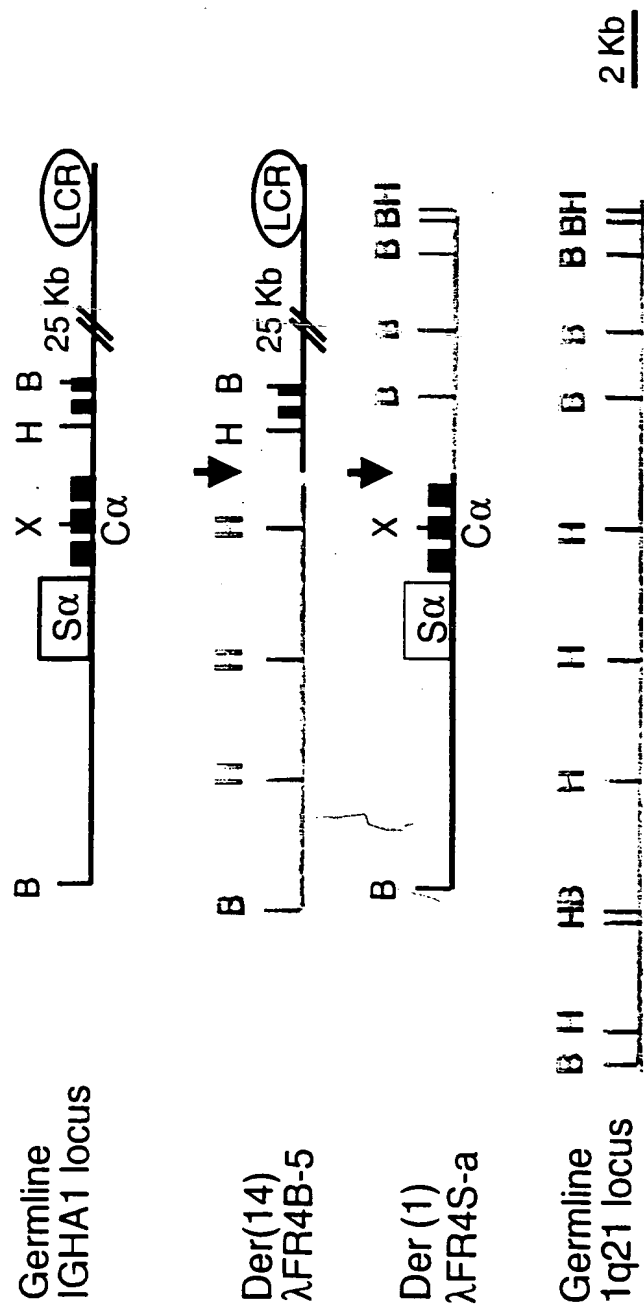


FIGURE 1



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FIG.1B

Chr 1 GGGCCTGACAGCAACITTTCTTCTACTAGTTTCATCTTAACCTTATCCTGGTAAC'TGGCGAGACAACCTGTCTTAAGTAACTGAAGGAAA
 |||||
 der14 GGGCCTGACAGCAACITTTCTTCTACTAGTTTCATCTTAACCTTATCCTGGTAACCTGAAGGAAA
 |||||
 Chr 14 TCCCACTGACGCATGCAGGAAGGGGCACCTCCCTTAACTGACACTGCTCTGTACGGGGCACAGGTGCACACTCACA

FIGURE 2A

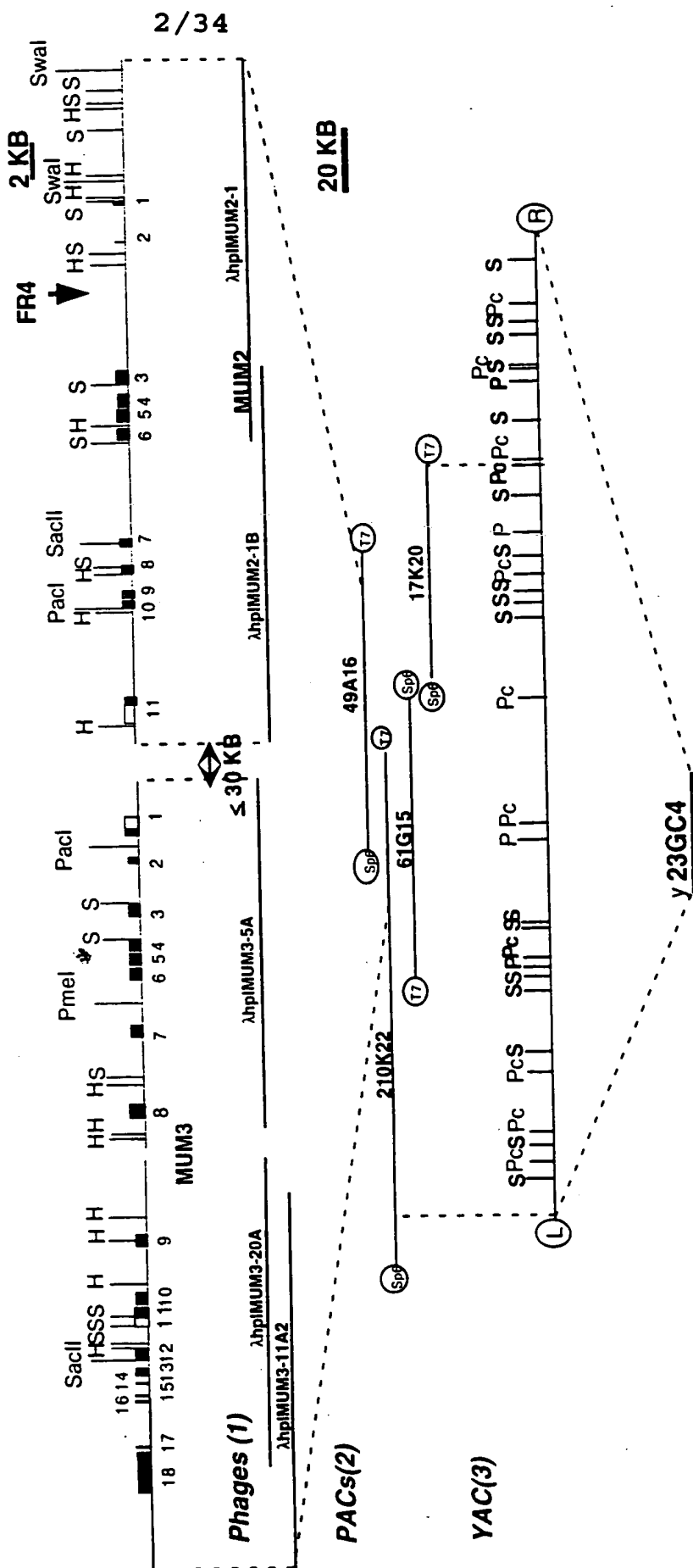


FIGURE 2B

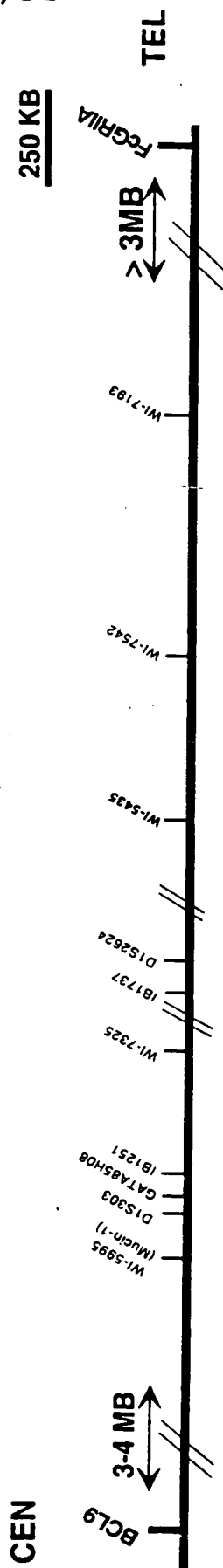


FIGURE 3

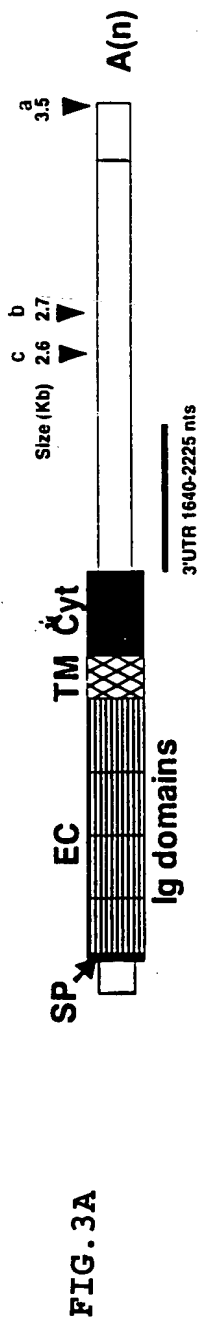


FIG. 3B

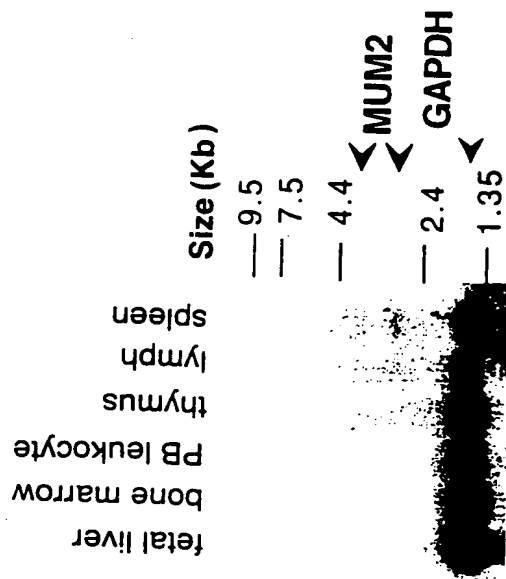
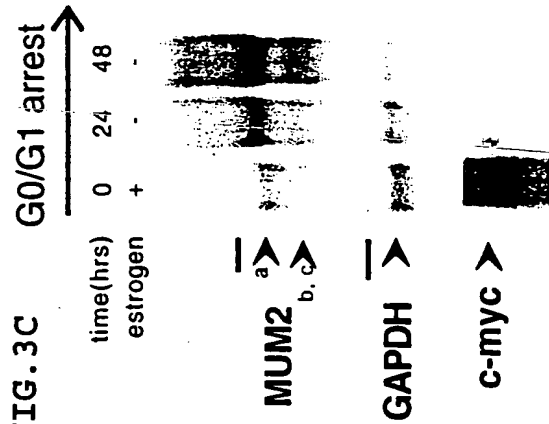


FIG. 3C



Quantitation of MUM2(a) mRNA levels

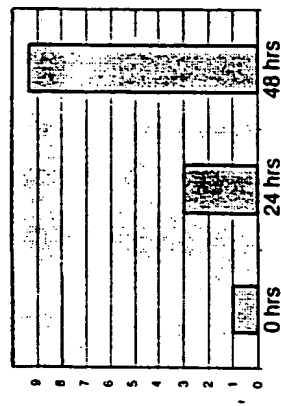


FIGURE 4

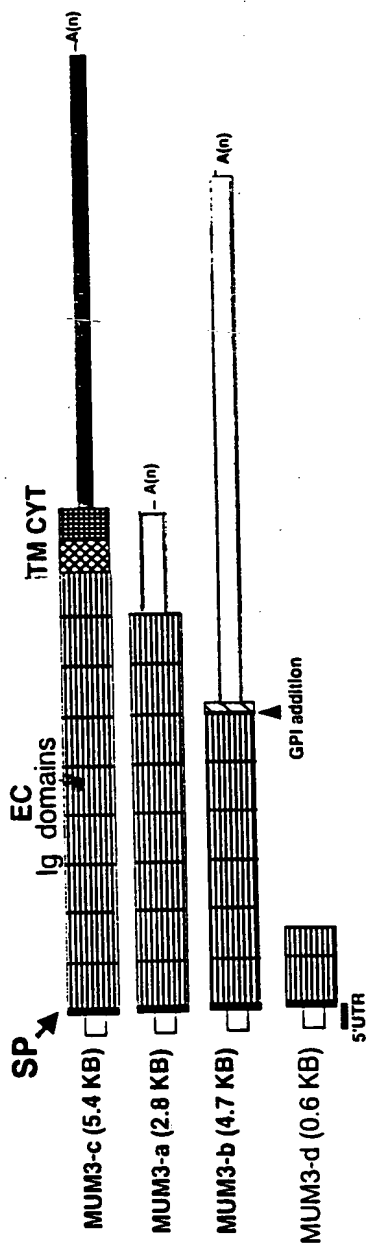


FIG. 4B

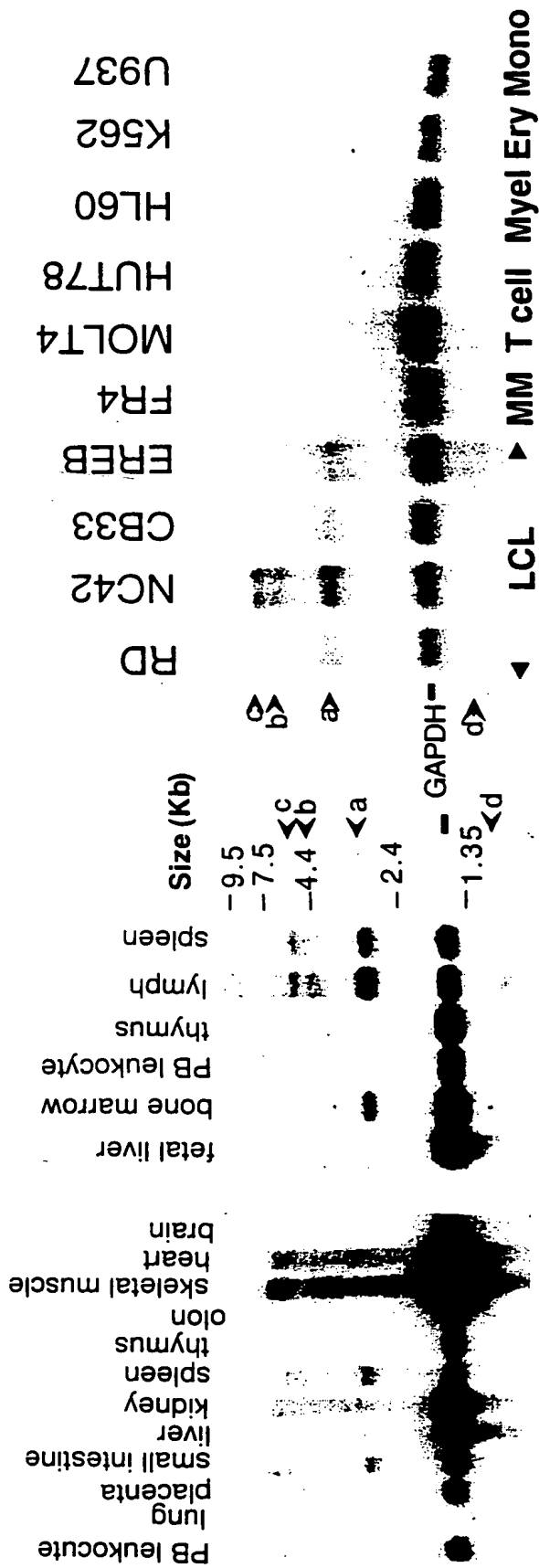


FIGURE 5

1 CTCAATCAGCTTTATGCAGAGAAGAAGCTTACTGAGCTCACTGCTGGTGGTGGTGTAGGCAAGTCTGCTTTGGCAA
 78 TCTGGGCTGACCTGGCTTGTCTCCTCAGAACTCCTTCTCCAACCCTGGAGCAGGCTTCCATGCTGCTGTGGGCGTCC M L L W A S
 155 TTGCTGGCCTTTGCTCCAGTCTGTGGACAATCTGCAGCTGCACACAAACCTGTGATTTCCGTCCATCCTCCATGGAC L L A F A P V C G Q S A A A H K P V I S V H P P W T 32
 232 CACATTCTTCAAAGGAGAGAGAGTGAAGTCTGACTTGAATGGATTTCAGTTCTATGCAACAGAGAAAACAATGGT T F F K G E R V T L T C N G F Q F Y A T E K T T W Y 58
 309 ATCATCGGCACTACTGGGGAGAAAAGTTGACCCTGACCCAGGAAACACCCTCGAGGTTCTGGGAATCTGGACTGTAC H R H Y W G E K L T L T P G N T L E V R E S G L Y 83
 386 AGATGCCAGGCCCGGGCTCCCCACGAAGTAACCCTGTGCGCTTGTCTTTTCTTCAGACTCCTTAATCCTGCAAGG R C Q A R G S P R S N P V R L L F S S D S L I L Q A 109
 463 ACCATATTCTGTGTTTGAAGGTGACACATGGTCTGAGATGCCACAGAAGAAGGAAAGAGAAATTGACTGCTGTGA P Y S V F E G D T L V L R C H R R R K E K L T A V K 135
 540 AATATACTTGAATGGAACATTTCTTTCCATTTCTAATAAAGCTGGGATCTTCTTATCCACAAGCAAGTTCAAAT Y T W N G N I L S I S N K S W D L L I P Q A S S N 160
 617 AACAAATGGCAATTATCGATGCATTGGATATGGAGATGAGAATGATGATTTAGATCAAATTTCAAATAATTAAAT N N G N Y R C I G Y G D E N D V F R S N F K I I K I 186
 694 TCAAGAACTATTTCCACATCCAGAGCTGAAAGCTACAGACTCTCAGCCTACAGAGGGGAATTCTGTAAACCTGAGCT Q E L F P H P E L K A T D S Q P T E G N S V N L S C 212
 771 GTGAACACAGCTTCTCCAGAGCGGTGAGACACCCCACTTCACTTCAACTTCTTCAGAGATGGCGAGGTCATCTG E T Q L P P E R S D T P L H F N F F R D G E V I L 237
 848 TCAGACTGGAGCAGTACCCGGAACCTCAGCTCCCAACCGTCTGGAGAGAAAACCTCAGGATCCTATTGGTGTGGTGC S D W S T Y P E L Q L P T V W R E N S G S Y W C G A 263
 925 TGAACAGTGAAGGGTAACATCCACAAGCAGCTCCCTCGCTACAGATCCATGTGCAGCGGATCCCTGTGTCTGGGG E T V R G N I H K H S P S L Q I H V Q R I P V S G V 289
 1002 TGCTCCTGGAGACCCAGCCCTCAGGGGGCCAGGCTGTTGAAGGGGAGATGCTGGTCTTGTCTGCTCCGTGGCTGAA L L E T Q P S G G Q A V E G E M L V L V C S V A E 314
 1079 GGCACGGGATACCATTTCTCTGGCAGGAGGATGCAGGAGAGTCTGGGGAGGAAAACCTCAGCGTTCCCT G T G D T T F S W H R E D M Q E S L G R K T Q R S L 340
 1156 GAGAGCAGAGCTGGAGCTCCCTGCCATCAGACAGAGCCATGCAGGGGATACTACTGTACAGDANAS Y G R A E L E L P A I R Q S H A G G Y C T A D N S Y G 366
 1233 GCCCTGTCCAGAGCATGGTGTGAATGTCACTGTGAGAGAGACCCCAAGCAACAGAGATGGCCTTGTGCGCCGCGGA P V Q R G N I H K H S P S L Q I H V Q R I P V S G V 391
 1310 GCCACTGGAGGGCTGCTCAGTCTTCTTCTGGCTGGCCCTGCTGTTTCACTGTGGCTGGGAGGAGTCAAG A T G G L L S A L L L A V A L L F H C W R R R K S G 417
 1387 AGTTGGTTTCTTGGGAGACGAAACCAGGCTCCCTCCCGCTCAGGCCCAGGAGAGTCTCCCATTCATCTGCCCTG V G F L G D E T R L P P A P G P G E S S H S I C P A 443
 1464 CCCAGGTGGAGCTTCAGTCGTGTATGTTGATGTACACCCCAAAAGGGAGATTGGTATACTCTGAGATCCAGACT Q V E L Q S L Y V D V H P K K G D L V Y S E I Q T 468
 1541 ACTCAGCTGGGAGAAGAAGAGGAAGCTAATACCTCCAGGACACTTCTAGAGGATAAGGATGTCTCAGTTGTCTACTC T Q L G E E E E A N T S R T L L E D K D V S V V Y S 494
 1618 TGAGGTAAAGACACAACACCCAGATAACTCAGCTGGAAGATCAGCTCTAAGGATGAAGAAAGTTAAGAGAATGAAA E V K T Q H P D N S A G K I S S K D E E S * 515
 1695 AGTTACGGGAACGTCTACTCATGTGATTTCTCCCTTGTCCAAAGTCCCAGGCCAGTGCAGTCTTGGCGCACCTG
 1772 GAATGATCAACTCATTCCAGCTTTCTAATTTCTCATGCATATGCATTCATCCAGGAATACTCATTGCTCTACT
 1849 CTGATGTTGGGATGGAATGGCCTCTGAAAGACTTCACTAAATGACAGGATCCACAGTTAAGAGAAGACCCCTGTAG
 1926 TATTGCTGTGGGCCTGACCTAATGCATTCCTAGGGTCTGCTTTAGAGAAGGGGGATAAAGAGAGAGAAGGACTGT
 2003 TATGAAAAACAGAAGCACAATTTTGGTGAATTGGGATTGTCAGAGATGAAAAAGACTGGGTGACCTGGATCTCTGC
 2080 TTAATACATCTACAACCATTTGTCTCACTGGAGACTCACTTGCATCAGTTTGTGTTAACTGTGAGTGGCTGCACAGGCA
 2157 GTGTGCAAAACAATGAAAAGCCCTTCACTTGTGCTGCACAGCTTACACTGTGAGGATTCAGTTGCAGATTAAGAA
 2234 CCCATCTGGAATGGTTTACAGAGAGAGGAATTTAAAAGAGGACATCAGAAGAGCTGGAGATGCAAGCTTAGGCTGC
 2311 GCTTCCAAAAGCAAATGATAATTATGTTAATGTCAATTAGTGACAAAGATTGCAACATTAGAGAAAAGAGACACAAA
 2388 TATAAAATTAATAAATTAAGTACCAACTCTCCAAAATAAATTGAACCTTAAATATTAGTATAAACTCATAATAAA
 2465 CTCTGCCTTTAAATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 6a

1 CGGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTTGGAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTG
 M L L W V I L L V L A P V S G ▼ Q F A R T P R 22
 81 GTGGTCCAGGTCTTCATGCTGCTGTGGGTGATATTACTGGTCTGGCTCCTGTGAGTGGACAGTTTGCAAGGACACCCAG
 P I I F L Q P P W T T V F Q G E R V T L T C K G F R F 49
 161 GCCCATTATTTTCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTACCCTCACTTGCAAGGGATTTTCGCT
 Y S P Q K T K W Y H R Y L G K E I L R E T P D N I L 75
 241 TCTACTCACCACAGAAAACAAATGGTACCATCGGTACCTTGGGAAAGAAATACTAAGAGAAACCCAGACAATATCCTT
 E V Q E S G E Y R C Q A Q G S P L S S P V H L D F S S 102
 321 GAGGTTTCAGGAATCTGGAGAGTACAGATGCCAGGCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTC
 A S L I L Q A P L S V F E G D S V V L R C R A K A E V129
 401 AGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGACTCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAG
 T L N N T I Y K N D N V L A F L N K R T D F H I P H 155
 481 TAACACTGAATAATACTATTTACAAGAATGATAATGCTCTGGCATTCTTAAATAAAAGAACTGACTTCCATATTCCTCAT
 A C L K D N G A Y R C T G Y K E S C C P V S S N T V K 182
 561 GCATGTCTCAAGGACAATGGTGCATATCGCTGTACTGGATATAAGGAAAGTTGTGCCCTGTTTCTTCCAATACAGTKAA
 I Q V Q E P F T R P V L R A S S F Q P I S G N P V T L209
 641 AATCCAAGTCCAAGAGCCATTTACACGTCCAGTGTGAGAGCCAGCTCCTTCCAGCCCATCAGCGGGAACCCAGTGACCC
 T C E T Q L S L E R S D V P L R F R F F R D D Q T L 235
 721 TGACCTGTGAGACCCAGCTCTCTAGAGAGGTGAGATGTCCCGCTCEGGTTCCGCTTCTTTCAGAGATGACCAACCCCTG
 G L G W S L S P N F Q I T A M W S K D S G F Y W C K A 262
 801 GGATTAGGCTGGAGTCTCTCCCCGAATTTCCAGATTACTGCCATGTGGAGTAAAGATTGAGGTTCTACTGGTGTAAAGGC
 A T M P H S V I S D S P R S W I Q V Q I P A S H P V L289
 881 AGCAACAATGCCTCAGAGCGTCATATCTGACAGCCCCAGATCCTGGATACAGGTGCAGATCCCTGCATCTCATCTGTCC
 T L S P E K A L N F E G T K V T L H C E T Q E D S L 315
 961 TCACTCTCAGCCCTGAAAAGGCTCTGAATTTTGAAGGAACCAAGGTGACACTTCACTGTGAAACCCAGGAAGATTCTCTG
 R T L Y R F Y H E G V P L R H K S V R C E R G A S I S 342
 1041 CGCACTTTGTACAGGTTTTATCATGAGGTGTCCCCCTGAGGCACAAGTCAGTCCGCTGTGAAAGGGGAGCATCCATCAG
 F S L T T E N S G N Y Y C T A D N G L G A K P S K A V369
 1121 CTTCTCACTGACTACAGAGAATTCAGGGAATCTACTGACAGCTGACAATGGCCTTGGCGCCAAGCCAGTAAGGCTG
 S L S V T V P V S H P V L N L S S S P E D L I F E G A 395
 1201 TGAGCCTCTCAGTCACTGTTCCCGTGTCTCATCTGTCTCAACCTCAGCTCTCTGAGGACCTGATTTTTGAGGGAGCC
 K V T L H C E A Q R G S L P I L Y Q F H H E D A A L E 422
 1281 AAGGTGACACTTCACTGTGAAGCCCAGAGAGGTTCACTCCCCATCCTGTACCAGTTTCATCATGAGGATGCTGCCCTGGA
 R R S A N S A G G V A I S F S L T A E H S G N Y Y C T449
 1361 GCGTAGGTGCGGCCACTGTCAGGAGGAGTGCCATCAGTTCTCTGACTGCAGAGCATTGAGGGAATCTACTGCA
 A D N G F G P Q R S K A V S L S I T V P V S H P V L 475
 1441 CAGCTGACAATGGCTTTGGCCCCCAGCGCAGTAAGGCGGTGAGCTCTCCATCACTGTCCCTGTGTCTCATCTGTCTCTC
 T L S S A E A L T F E G A T V T L H C E V Q R G S P Q 502
 1521 ACCCTCAGCTCTGTGAGGCCCTGACTTTTGAAGGAGCCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCCCACA
 I L Y Q F Y H E D M P L W S S S T P S V G R V S F S 529
 1601 AATCCTATACCAGTTTTATCATGAGGACATGCCCCGTGTGGAGCAGCTCAACACCCTCTGTGGGAAGAGTGTCTTTCAGCT
 S L T E G H S G N Y Y C T A D N G F G P Q R S E V V 555
 1681 TCTCTCTGACTGAAGGACATTCAGGGAATTACTACTGCACAGCTGACAATGGCTTTGGTCCCCAGCGCAGTGAAGTGGTG
 S L F V T V P V S R P I L T L R V P R A Q A V G D L 582
 1761 AGCCTTTTGTCACTGTTCCAGTGCTCGCCCATCCTCACCCTCAGGGTTCCAGGGCCAGGCTGTGGTGGGGGACCT
 L E L H C E A P R G S P P I L Y W F Y H E D V T L G 609
 1841 GCTGGAGCTTCACTGTGAGGCCCCGAGAGGCTCTCCCCAATCCTGTACTGGTTTTATCATGAGGATGTCACCCTGGGGA
 S S A P S G G E A S F N L S L T A E H S G N Y S C E 635
 1921 GCAGCTCAGCCCCCTCTGGAGGAGAAGCTTCTTTCAACCTCTCTGACTGCAGAACATTCTGGAACCTACTCATGTGAG
 A N N G L V A Q H S D T I S L S V I V P V S R P I L T 662
 2001 GCCAACAATGGCCTAGTGGCCAGCAGTACACAATATCACTCAGTGTATAGTTCCAGTATCTCGTCCCATCCTCAC
 F R A P R A Q A V V G D L L E L H C E A L R G S S P I689
 2081 CTTTCAGGGCTCCCAGGGCCCAGGCTGTGGTGGGGGACCTGCTGGAGCTTCACTGTGAGGCCCTGAGAGGCTCCTCCCCAA
 L Y W F Y H E D V T L G K I S A P S G G G A S F N L 715
 2161 TCCTGTACTGGTTTTATCATGAAGATGTCACCCTGGGTAAGATCTCAGCCCTCTGAGGAGGGGCTCCTTCAACCTC
 S L T T E H S G I Y S C E A D N G L E A Q R S E M V T 742
 2241 TCTCTGACTACAGAATCTGGAATCTACTCCTGTGAGGCAGACAATGGTCTGGAGGCCAGCGCAGTGAGATGGTGAC
 L K V A G E W A L P T S S T S E N * 759
 2321 ACTGAAAGTTGCAGGTGAGTGGGCCCTGCCACCAGCAGCACATCTGGAACCTGACTGTGCCTGTTCTCCTGCAGCTGA
 2401 AAATGGAGCCACAGAGCTCCTCAGGGCTGTTTGTGTGTGGCATCCAGCACACTTCTGCCTGCAGAACCTCCTGTG
 2481 AAAGTCTCGGATCCTTTGTGGTATGGTTCCAGGAATCTGATGTTTCCAGCAGTCTTCTTGAAGATGATCAAAGCACCTC
 2561 ACTAAAAATGCAATAAGACTTTTTTGAACATAAACTATATTCTGAACTGAAATTATTACATGAAATGAAACCAAGA
 2641 ATTCTGAGCATATGTTTCTCTGCGTAGAAAGGATTAAGCTGTTTCTGTCCGATTCTTCTCTATTGACTTCTAAGAA
 2721 GCCTCTACTCTTGAGTCTCTTTCATTAAGTGGGATGTAATGTTCTTACATTTCACATTAATAATCCTATGTTAACGA
 AAAAA

FIGURE 6b

1 CGGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTTGGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTG
 M L L W V I L L V L A P V S G Q F A R T P R 22
 81 GTGGTCCAGGTCTTCTGCTGTGGGTGATATTACTGGTCTGGCTCTGTGCTGAGTGGACAGTTTGAAGGACACCCAG
 P I I F L Q P P W T T V F Q G E R V T L T C K G F R F 49
 161 GCCCATTATTTTCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCTCACTTGAAGGGATTTCGCT
 Y S P Q K T K W Y H R Y L G K E I L R E T P D N I L 75
 241 TCTACTCACCACAGAAAACAAATGGTACCATCGGTACCTTGGGAAAGAAATACTAAGAGAAACCCAGACAATATCCTT
 E V Q E S G E Y R C Q A Q G S P L S S P V H L D F S S 102
 321 GAGGTTCAAGAACTGAGAGTACAGATGCCAGGCCAGGGCTCCCTCTCAGTAGCCCTGTGCACCTTGGATTTCCTT
 A S L I L Q A P L S V F E G D S V V L R C R A K A E V 129
 401 AGCTTCGCTGATCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGACTCTGTGGTTCTGAGGTGCCGGGCAAGCGGAAG
 T L N N T I Y K N D N V L A F L N K R T D F H I P H 155
 481 TAACACTGAATAATACTATTACAAGATGATAATGCTCTGGCATTCTTAATAAAGAACTGACTTCCATATTCCTCAT
 A C L K D N G A Y R C T G Y K E S C C P V S S N T K V K 182
 561 GCATGTCTCAAGGACAATGGTGCATATCGCTGTACTGGATATAAGGAAAGTTGTTGCCCTGTTTCTTCCAATACAGTCAA
 I Q V Q E P F T R P V L R A S S F Q P I S G N P V T L 209
 641 AATCCAAGTCCAAGAGCCATTTACAGCTCCAGTCTGAGAGCCAGTCTCTCCAGCCCATCAGCGGGAACCCAGTGACCC
 T C E T Q L S L E R S D V P L R F R F R D D Q T L 235
 721 TGACCTGTGAGACCCAGTCTCTCTAGAGAGGTGAGATGTCCCGTCCGGTTCGGTTCCTCAGAGATGACCAGACCCGTG
 G L G W S L S K F Q I T A M W S K D S G F Y W C K A 262
 801 GGATTAGGCTGGAGTCTCTCCCGAATTTCAGATTACTGCCATGTGGAGTAAAGATTGAGGGTCTACTGGTGTAAAGGC
 A T M P H S V I S D S P R S W I Q V Q I P A S H P V L 289
 881 AGCAACAATGCTCAGAGCTCATATCTGACAGCCGAGATCTGGATACAGGTGAGATCCCTGCATCTCATCTCTCTC
 T L S P E K A L N F E G T K V T L H C E T Q E D S L 315
 961 TCACTCTCAGCCCTGAAAAGGCTCTGAATTTGAGGGAACCAAGGTGACACTTCACTGTGAAACCCAGGAAGATTCTCTG
 R T L Y R F Y H E G V P L R H K S V R C E R G A S I S 342
 1041 CGCACTTTGTACAGGTTTATCATGAGGTGTCCCGTGGGCAAGTCAAGTCCGCTGTGAAAGGGGAGCATCCATCAG
 F S L T T E N S G N Y Y C T A D N G L G A K P S K A V 369
 1121 CTTCTCACTGACTACAGAGAATTCAAGGAACTACTACTGCACAGTGCACATGGCCTTGGCGCAAGCCAGTAAGGCTG
 S L S V T V P V S L N L S S P E D L I F E G A 395
 1201 TGAGCCTCTCAGTCACTGTTCCCGTGTCTCATCTGTCTCAACCTCAGCTCTCTGAGGACCTGATTTTGAGGAGGCC
 K V T L H C E A Q R G S L P I L Y Q F H H E D A A L E 422
 1281 AAGGTGACACTTCACTGTGAAGCCAGAGAGGTTCATCTCCCATCTGTACCAGTTTCATCATGAGGATGCTGCCCTGGA
 R R S A N S A G V A I S F S L T A E H S G N Y Y C T 449
 1361 GCGTAGGTGCGCCAACTCTGCAGGAGGAGTGGCCATCAGCTTCTCTCTGACTGCAGAGCATTAGGGAACCTACTACTGCA
 A D N G F G P Q R S K A V S L S I T V P V S H P V L 475
 1441 CAGCTGACAAATGGCTTTGGCCCGCAGTAAAGCGGTGAGGCTCTCCATCACTGTCCCTGTGTCTCATCTGTCTCTC
 T L S S A E A L T F E G A T V T L H C E V Q R G S P Q 502
 1521 ACCCTCAGCTCTGTGAGGCCCTGACTTTTGAAGGAGCCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCCCACA
 I L Y Q F Y H E D M P L H S S S T P S V G R V S F S F 529
 1601 AATCTTATACAGTTTATCATGAGGACATGCCCTGTGAGGAGCTCAACACCCCTCTGTGGGAAGAGTGTCTTCACT
 S L T E G H S G N Y Y C T A D N G F G P Q R S E V V 555
 1681 TCTCTGACTGAAGGACATTCAAGGAATTACTACTGCACAGTGCACATGGCTTTGGTCCCCAGCGCAGTGAAGTGGTG
 S L F V T G K C W V L A S H P P L A E F S L T H S F K 582
 1761 AGCCTTTTGTCACTGGTAAGTGTGGGTCTTGGCAGTCAACCCCTGGCTGAGTCTCTCTCAACCATTCCTTTAA
 N L F A L S S F L P * stop 592
 1841 AAATCTGTTTGCAGTGTCCAGTTTCTCCCTAATCAACTTAATCCCTTCTTGGCTTCTCTCAACTAAGTCTGGG
 1921 GTTTTCCGTACTCATAAGTCTGTGCTCAGCCAGACCCCTAAAACAGCTCAGTAGATTCCCAGCTTTTACCAATGAATT
 2001 TATTATTGTATTTTCTCTCATTCCTGTATGTTTCCAACAGTACGCCAATTTTCTTGATGCAGGAGCGTGTCTTACT
 2081 TCTCTACTGACATTTACATATTAATCTAGCTACAAGCAGCTCTATAGATAAATATTGGTCAAGACCTTAAATCTCCA
 2161 AAGGATTTCCAATCTTATGGTAGATTGGGAGAAAGCTGCTGGTGAACAAAGGGGAAATGGCTCCCTAGGAACCAACTCC
 2241 TCAAACTCTGGAGTTTTTATGATCCCTTGTTTTCTAACTGCTAAAATCAGTATCATTTTATTGTATTATTTTAAAAAA
 2321 ACTATTGTTGAAGTATGACATACATTCAAGAAACGTGTCAAAATGTATGTGTACGATTGGTGTCTTTTAGGAGCTAA
 2401 GTTGCTTCTGTTTTACTTGAATCTTTGTTTATAGAAACTGGGGGAAAGTTACTTTCTTTTTCAGAGAAGCCAAATGTA
 2481 TGATAGAAAAATCTTGAGCCTGATGTGTGACATGCCCCTAGCATAACTTGTGAGTAAAGAGGTTATTTTAAATGT
 2561 GAATGTTCTGAGACTACTCCAAAGTCAGAGCCAAATCTACTAGGAAGCTTCTAGACTTCACTCATCTGCATCCCATTC
 2641 TACTTTTTTATCCATGTTTACTTTCTCATATTCTCAGCAGCATCTTAAGCCTCTTATTCTTGTCTTCTGACTGTCA
 2721 CCCTTAATGCCAGTAGAATGTAAGCTTCATGAGAACGAACTGCATCCATCTTGGTCTTCACAACATCCCTGTGCTACT
 2801 CAGTGTGTTGGCACACAGTAGGTCTCAGTCAACATTTGTAATTTAGTGGACAGATGATATGACAAGATGATAAGAGGGGA
 2881 TTTAAAAAATCATCTAGCAAAGCCCAAGAGGAAAAAACAAGCTATTTAGAAATGAAATACCAATTTGAAGCAGTA
 2961 AGAATAGATTGGATATCTTTGAAAACCATTAATTGAATGAAGAACAATTTGAGAAAACAATACAGAATGCAAGTAGAA
 3041 AGATACAGAAATAAAGGCAAAAGTTATAATATGGAATCAGACAAATGGATTGTCTGTATCCAGTTATGTGGATAATTAA
 3121 AATGGAGACCCCTCAGAAAATTGAACCGAAGAGTAAATGAAACTCAAAAATGTAGTAGAAATTTGTTGGGAAGTAAAGAAA
 3201 ACTTGAATATGTAGATCAGAACATATATGTTGATGACGTTATTTGACTTTGAGGTTAAAAATATATATATGTGCTTATGAT
 3281 TATGGGAAAAAAGCAGTCTGCTCAGAAAGAAAAACATCAAGTTAGTCTTAGACTTTGCACTGCACTCAGTACCAAGAG
 3361 AGAGGAGGCCAGACTTGGACCTGCGAGGGAAGAATAATACCCGAAAAATTTATATCAATCAAAAAGACATTTGCAAAAA
 3441 TACAGGATTTCAGGAACTGAGAACTGCACTAAGCCTTCTGGAACCAACACCTAATGACAAAATCTAGCCCAACAAAGTGT
 3521 AAATGAATATAAAGGACTCATAATGAGGAAACCGCATTATGACTGGCTCTCAACCTGGCCGCATATTAGACTCGTCAAA
 3601 GACCTTTGTAAGAGGTACACATGACTCGTCAAGGCCCTCTCCAGACTAATCAATTCAGAATCTCAGAGATGGGGCC
 3681 ACAGAATCAGTATTTTGGACAACTCAAGTGAGAATTATGTGTAGACAAGATTGGAACCACTGATTATGATATAGA
 3761 AACAAAGGCTAATCAACTGTGAGAATTATGGTACAGAATGAAGTAACATTTATGAACACTGAAATGTAAGAAAAAT
 3841 GTAACAAAGAAAAATAGTTAGAGGAAGGAGGAGGAGTAAAGGAACAATCATTTTCTCATGATTATTTATTTTCAAGAGTA
 3921 AATTGTGAGTTATTTTCAATTCAAAAAGAAATGGACTTTTTTAAAAAATTAGTAATAGATTTCAAAATGTCCATTTTGTA
 4001 AATCGTTTCTGAATACTTTGTCAACAGTTACTCATATTAATGGCTTACTTCACTAAAATTCATGGAAAACCAACTA
 4081 TAGCCTGTAGAGTACATAGGAGAGAACAAGTGAATCTTTGGGTGGCGCAAGCATAGATGTTAGGACTGACAAAAAA
 4161 AATAATAAAAAATAAACCCTGTGCATTGATATGATCAAAATGATCAGGGAAGAGGAAACAGAAACTCATCAACGCCATTA
 4241 TTACAAGTGTAAATTTGGTTCAACCTTTTCGTCTTAATTGACACATTGTAATGTATATATTTATGGAAGCACAGTTTGAT
 4321 ATTTTGATATACATACATGTTATATAACGATCAAATTAGGATATTTAATGTACCCATCATCTCATGCAATTTATCATTTCT
 4401 TTGGAATAAA AACATTCAA AGCCAAAAA AAAAAA AAAAAA

FIGURE 6c-1

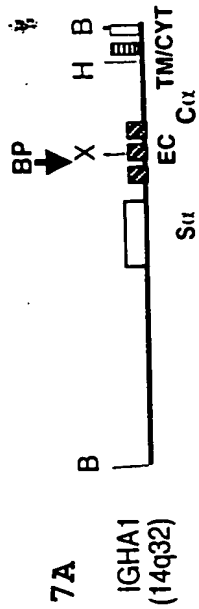
1 CGGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTTGGAATTGAGGAACTCTCTTTTATCTCAGCCCTTG
 M L L W V I L L V L A P V S G Q F A R T P R 22
 81 GTGGTCCAGGTCTTCATGCTGCTGTGGGTGATATTACTGGTCTGGCTCCTGTCTAGTGGACAGTTTGCAAGGACACCCAG
 P I I F L Q P P W T T V F Q G E R V T L T C K G F R F 49
 161 GCCCATTATTTTCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGTGACCCTCACTTGCAAGGGATTTCGCT
 Y S P Q K T K W Y H R Y L G K E I L R E T P D N I L 75
 241 TCTACTCACCACAGAAAACAAATGGTACCATCGGTACCTTGGGAAAGAAATACTAAGAGAAACCCAGACAATATCCTT
 E V Q E S G E Y R C Q A Q G S P L S S P V H L D F S S 102
 321 GAGGTTCCAGGAATCTGGAGAGTACAGATGCCAGGCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTCCTTC
 A S L I L Q A P L S V F E G D S V V L R C R A K A E V 129
 401 AGCTTCGCTGATCTGCAAGCTCCACTTTCTGTGTTGAAGGAGACTCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAG
 T L N N T I Y K N D N V L A F L N K R T D F H I P H 155
 481 TAACACTGAATAACTATTACAGAATGATAATGTCTGGCATTCCTTAATAAAAGAACTGACTTCCATATTCCTCAT
 A C L K D N G A Y R C T G Y K E S C C P V S S N T V K 182
 561 GCATGTCTCAAGGACAATGGTGCATATCGCTGTACTGGATATAAGGAAAGTTGTTGCCCTGTTTCTTCCAATACAGTCAA
 I Q V Q E P F T R P V L R A S S S F Q P I S G N P V T L 209
 641 AATCCAAGTCCAAGAGCCATTTACACGTCCAGTGTCTGAGAGCCAGCTCCTTCCAGCCCATCAGCGGGAACCCAGTGACCC
 T C E T Q L S L E R S D V P L R F R F R F R D L 235
 721 TGACCTGTGAGACCCAGCTCTCTCTAGAGAGGTGAGATGTCCCGCTCCGGTTCCGCTTCTTCTAGAGATGACCAGACCTG
 G L G W S L S P N F Q I T A M W S K D S G F Y W C K A 262
 801 GGATTAGGTGGAGTCTCTCCCGAATTTCCAGATTAAGTGTGAGTAAAGATTGAGGGTTCTAGGGTGAAGGC
 A T M P H S V I S D S P R S W I Q V Q I P A S H P V L 289
 881 AGCAACAATGCCTCACAGGCTCATATCTGACAGCCGAGATCCTGGATACAGGTGCAGATCCCTGCATCTCATCTCTGCC
 T L S P E K A L N F E G T K V T L H C E T Q E D S L 315
 961 TCACTCTCAGCCCTGAAAAGGCTCTGAATTTGAGGGAACCAAGGTGACACTTCACTGTGAACCCAGAGATTCTCTG
 R T L Y R F Y H E G V P L R H K S V R C E R G A S I S 342
 1041 CGCATTCTTACAGGTTTTATCATGAGGGTGTCCCTTGAAGGCAAGTCAGTCCGCTGTGAAAGGGGAGCATCCATCAG
 F S L T T E N S G N Y Y C T A D N G L G A K P S K A V 369
 1121 CTTCTCACTGACTACAGAGAATTCAGGGAATCTACTGACAGCTGACAATGGCCTTGGCGCCAAGCCAGTAAGGCTG
 S L S V T V P V S H P V L N L S S P E D L I F E G A 395
 1201 TGAGCCTCTCAGTCACTGTCTCCGCTGTCTCATCTGTCTCAACCTCAGCTCTCTGAGGACCTGATTTTGAAGGAGCC
 K V T L H C E A Q R G S L P I L Y Q F H E D A A L E 422
 1281 AAGGTGACACTTCACTGTGAAGCCAGAGAGGTTCACCTCCCATCTGTACAGTTTCATCATGAGGATGCTGCCCTGGA
 R R S A N S A G G V A I S F S L T A E H S G N Y Y C T 449
 1361 GCGTAGGTGCGGCCAATCTGACGAGGAGTGGCCATCAGCTTCTCTCTGACTGCAGAGCATTGAGGGAATCACTACTGCA
 A D N G F G P Q R S K A V S L S I T V P V S H P V L 475
 1441 CAGCTGACAATGGCTTTGGCCCCAGCGCAGTAAGGCGGTGAGCCTCTCCATCACTGTCCCTGTGTCTCATCTGTCTC
 T L S S A E A L T F E G A T V T L H C E V Q R G S P Q 502
 1521 ACCCTCAGCTCTGCTGAGGCCCTGACTTTTGAAGGAGCCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCCCACA
 I L Y Q F Y H E D M P L W S S S T P S V G R V S F S F 529
 1601 AATCTATACAGTTTATCATGAGGACATGCCCTGTGAGCAGTCAACACCCTCTGTGGGAAGAGTGTCTCTCAGCT
 S L T E G H S G N Y Y C T A D N G F G P Q R S E V V 555
 1681 TCTCTCTGACTGAAGGACATTGAGGAATTAAGTGTGACAGCTGACAATGGCTTTGGTCCCCAGCGCAGTGAAGTGGTG
 S L F V T V P V S R P I L T L R V P R A Q A V V G D L 582
 1761 AGCCTTTTGTCACTGTTCCAGTGTCTCGCCCCATCTCACCCTCAGGGTCCCAGGGCCAGGCTGTGGTGGGGGACCT
 L E L H C E A P R G S P P I L Y W F Y H E D V T L G S 609
 1841 GCTGGAGCTTCACTGTGAGGCCCGAGAGGCTCTCCCCAATCTGTACTGGTCTTATCATGAGGATGTCACTCCCTGGGGA
 S A P S G G A S F H L T A E H S G N Y S C E 635
 1921 GCAGCTCAGCCCCCTCTGGAGGAGAAGCTTCTTCAACCTCTCTCTGACTGCAGAACATTCTGGAATACTACTCATGTGAG
 A N N G L V A Q H S D T I S L S V I V P V S R P I L T 662
 2001 GCCAACAATGCGCTAGTGGCCAGCAGTGCACAAATATCACTAGTGTATAGTTCCAGTATCTCGTCCCATCTCAC
 F R A P R A Q A V V G D L L E L H C E A L R G S S P I 689
 2081 CTTCAAGGCTCCCAGGGCCAGGCTGTGGTGGGGGACCTGTGGAGCTTCACTGTGAGGCCCTGAGAGGCTCCTCCCCAA
 L Y W F Y H E D V T L G K I S A P S G G G A S F N L 715
 2161 TCTGTACTGGTTTTATCATGAAGATGTCACTCTGGTAAGATCTCAGCCCCCTCTGGAGGAGGGCCCTCTCAACCTC
 S L T T E H S G I Y S C E A D N G L E A Q R S E M V T 742
 2241 TCTCTGACTACAGAACATTCTGGAATCTACTCTGTGAGGCAGACAATGGTCTGGAGGCCAGCGCAGTGAGATGGTGAC
 L K V A V P V S R P V L T L R A P G T H A A V G D L L 769
 2321 ACTGAAAGTTGCAAGTCCGGTGTCTCGCCCGGTCTCACCCTCAGGGCTCCCGGGACCCATGTCTCGGTGGGGGACCTGC
 E L H C E A L R G S P L I L Y R F F H E D V T L G N 795
 2401 TGGAGCTTCACTGTGAGGCCCTGAGAGGCTCTCCCTGATCTGTACCGGTTTTTTCATGAGGATGTCACTCCAGGAAAT
 R S S P S G G A S L N L S L T A E H S G N Y S C E A D 822
 2481 AGGTCTGCCCCCTCTGGAGGAGCGTCTTAAACCTCTCTCTGACTGCAGAGCACTCTGGAATACTCTGTGAGGCCGA
 N G L G A Q R S E T V T L Y I T G L T A N R S G P F A 849
 2561 CAATGGCCTCGGGGCCAGTGCAGTGCAGACTTTATATCAAGGGCTGACCGGAGAGGAGTGTCCCTTTTGG
 T G V A G G G L L S I S G L A A G A L L L Y C W I S R 875
 2641 CCACAGGAGTCCCGGGGGCTGTCTAGCATAGCAGGCTTCTGCGGGGGCACTGCTGCTCTACTGCTGCTCTCGAGA
 K A G R K P A S D P A R S P S D S D S Q E P T Y H N V 902
 2721 AAAGCAGGGAGAAAGCCTGCCTCTGACCCCGCCAGGAGCCCTTCAGACTCGGACTCCCAAGAGCCCACTATCACAATGT
 P A W E E L Q P V Y T N A N P R G E N V V Y S E V R I 929
 2801 ACCAGCTGGGAAGAGTGAACCAAGTGTACATAAGTCAAACTAGAGGAGAAAATGTGTTTACTCAGAAGTACGGA
 I Q E K K K H A V A S D P R H L R N K G S P I I Y S 955
 2881 TCATCCAAGAGAAAAAGAACATGCAGTGGCCTCTGACCCAGGCATCTCAGGAACAAGGGTTCCCTATCATCTACTCT

FIGURE 6c-2

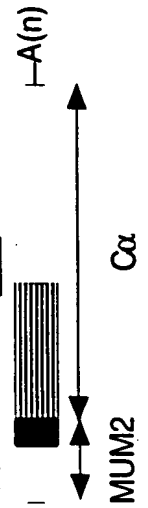
E V K V A S T P V S G S L F L A S S A P H R * stop 977

2961 GAAGTTAAGGTGGCGTCAACCCCGGTTTCCGGATCCCTGTTCTTGGCTTCCTCAGCTCCTCACAGATGAGTCCACACGTC
3041 TCTCCAACCTGCTGTTTCAGCCTCTGCACCCCAAAGTTCCTTGGGGGAGAAGCAGCATTGAAGTGGGAAGATTAGGCT
3121 GCCCCAGACCATATCTACTGGCCTTTGTTTCACATGTCTCATTCTCAGTCTGACCAGAATGCAGGGCCCTGCTGGACTG
3201 TCACCTGTTTCCAGTTAAAGCCCTGACTGGCAGGTTTTTTAATCCAGTGGCAAGGTGCTCCCACTCCAGGGCCAGCAC
3281 ATCTCCTGGATTCTTAGTGGGCTTCAGCTGTGGTGTCTGTTCTGAGTACTGCTCTCATCACACCCCCACAGAGGGGGTTC
3361 TTACCACACAAAGGAGAGTGGGCTTCAGGAGATGCCGGGCTGGCCTAACAGCTCAGGTGCTCCTAACTCCGACACAG
3441 AGTTCCTGCTTTGGGTGGATGCATTCTCAATTGTCATCAGCCTGGTGGGGCTACTGCAGTGTGCTGCCAAATGGGACAG
3521 CACACAGCCTGTGCACATGGGACATGTGATGGGTCTCCCCAGGGGGCTGCATTTACACTCCTCCACCTGTCTCAAACCT
3601 CTAAGGTCGGCACTTGACACCAAGGTAACCTCTCTCTGCTCATGTGTGCTAGTGTCTACCTGCCCAAGTAAGTGGCTTTCA
3681 TACACCAAGTCCCGAAGTTCTTCCCATCCTAACAGAAGTAACCCAGCAAGTCAAGGCCAGGAGGACCAGGGGTGCAGACA
3761 GAACACATACTGGAACACAGGAGGTGCTCAATTACTATTTGACTGACTGACTGAATGAATGAATGAATGAGGAAGAAAAC
3841 TGTGGGTAAATCAAACCTGGCATAAAATCCAGTGCCTCCCTAGGAAATCCGGGAGGTATTCTGGCTTCTCAAGAAACAACG
3921 GAAGAGAAGGAGCTTGGATGAAGAACTGTTGAGCAAGAAGAAGGCTTCTTCACACTTTTATGTGCTTGTGGATCACCT
4001 GAGGATCTGTGAAAATACAGATACTGATTGAGTGGGTCTGTGTAGAGCCTGAGACTGCCATTCTAACATGTTCCAGGGG
4081 ATGCTGATGCTGTGGCCCTGGGACTGCACTGCATGTCATGTAAGCCCTATAGGTCTCAGCAGAGGGCCATGGAGAGGGA
4161 ATGTGTGGCTCTGGCTGCCAGGGCCCACTCGGTTACACGGATCGTGTGCTCCTTGGCCAGCCTTTGGCCACAGCAC
4241 CACCAGCTGCTGTTGCTGAGAGAGCTTCTTCTCTGTGACATGTTGGCTTTTCATCAGCCACCCTGGGAAGCGGAAAGTAGC
4321 TGCCACTATCTTTGTTTCCCACTCAGGCCTCACACTTTCCCATGAAAAGGGTGAATGTATATAACCTGAGCCCTCTCC
4401 ATTCAGAGTTGTTCTCCCATCTCTGAGCAATGGGATGTTCTGTTCCGCTTTTATGATATCCATCACATCTTATCTTGATC
4481 TTTGCTCCCAGTGGATTGTACAGTGATGACTTTTAAGCCCCACGGCCTGAAATAAAATCCTTCCAAGGGCATTGGAAGC
4561 TCACTCCACCTGAACCATGGCTTTTCATGCTTCAAGTGTGAGGGCCTTGCCAGATAGACAGGGCTGACTCTGCTGCCC
4641 CAACCTTTCAAGGAGGAAACCAGACACCTGAGACAGGAGCCTGTATGCAGCCAGTGCAGCCTTGACAGGACAAAGGCTG
4721 GAGGCATTTGTCTACACTACAGATATGCAACTAAAATAGACGTGGAGCAAGAGAAATGCATTTCCACCGAGGCCGCTTTT
4801 TTAGGCCCTAGTTGAAAGTCAAGAAGGACAGCAGCAAGCATAGGCTCAGGATTAAAGAAAAAAATCTGCTCACAGTCTGTT
4881 CTGGAGGTACATCACCAACAAAGCTCACGCCCTATGCAGTCTGAGAAGGTGGAGGCACCAGGCTCAAAGAGGAAATT
4961 TAGAATTTCTCATTGGGAGAGTAAGGTACCCCATCCAGAATGATAACTGCACAGTGGCAGAACAACTCCACCCTAAT
5041 GTGGGTGGACCCCATCCAGTCTGTTGAAGGCCTGAATGTAACAAAAGGGCTTATTCTTCTCAAGTAAGGGGGAATCCT
5121 GCTTTGGGCTGGGACATAAGTTTTCTGCTTTTCAGACGCAAACTGAAAAATGGCTCTTCTTGGGTCTTGAGCTTGCTGGC
5201 ATATGGACTGAAAGAACTATGCTATTGGATCTCCTGGATCTCCAGCTTGCTGACTGCAGATCTTGAGATATGTCAGCCT
5281 CTACAGTCACAAGAGCTAATTCATTCTAATAAACCAATCTTTC

FIG. 7A



Probe: ex 1 MUM2

[illegible]

12/34

FIGURE 8A

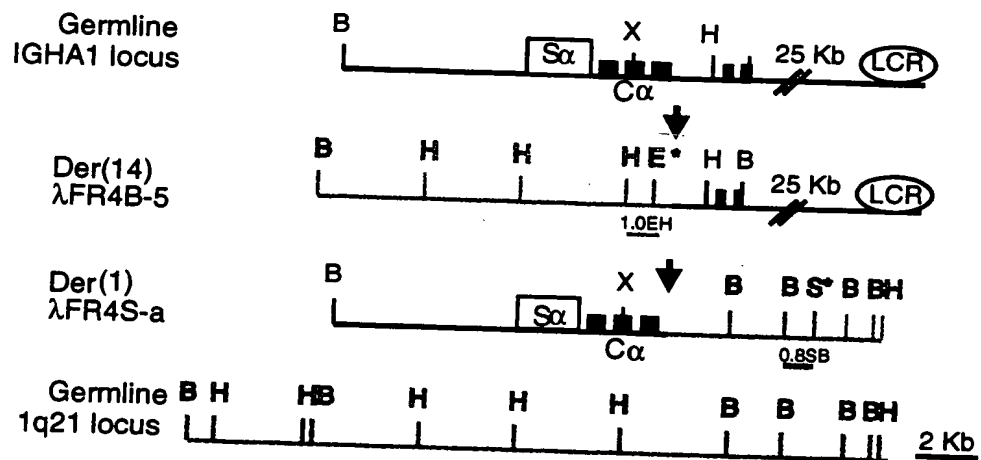


FIG. 8B

FIGURE 8

[illegible]

0.5 Kb



0.5 Kb



0.5 Kb

FIGURE 10

FIG. 10A

FCGR1IA (1) MAMETQMSQNVCPNFWLQPTVLLALLAALDGAAPFAAARAKLPPHIAVQAEVTHVTHVARSPEIDLOMFHKKIIPHQQSYRPFKANNKDK
 FCGR1IA (1) -----SQQLLFTALLLAAAGAKETEDLPAWFLFEPQYRWAKEKRWTHKGLAYSPDENMTQMFINEKIIQSSYFDATVTPAKG
 FCER1A (1) -----MAP-ALESPTLCAALDFAPDFVLVPOREKSGDNPNNRSPKSGENVTHTQNNFMSSTRMFINCEISSTSTSLNINNAKFPDPC
 FCGR1A (1) -----TWGMLALWPDVGV-DTTRAVISLCPNVVQGEAVTHVVLHFGCSTOMFLNATATSPYRITSASNDP
 IRTA1 (1) -----KLMWELLAAAPVCEGSAARAVIGVDPMTFFKTRVTHQNGFOYAEEXTTMMHYWCELLPGNT-LEQAEK
 IRTA2 (1) -----HLMWILAMAPVSGFARTPEZLIFQDPTVFOGRVTHQNGPREYEQTHVHYLGRKILREPDNI-LEVQAEK

FCGR1IA (101) EVTCTQISLSDIVATVLEWMLQADHLEPQKESWLRCHMKKPIKAVTAMONKQHSLLTETLIPAAHSHSEPTVTHNNTYTL-SKK
 FCGR1IA (86) EVKCCTLTASDIVCDEWHIEMLLQARWVKEDITHRCISGNNTATKAVTHQNGKQKSGHEDPYILKMAKUSEFVTRRLTSKN-VSE
 FCER1A (90) EVKCHQOVNESEPVVEMFEMMLLOAQAAYVMECPPIARCICDWDVKKVAKKCPKELHSGVPELTSIPATAVAREDEETAYVTRKMQLD-22E
 FCGR1A (82) EVKCCRLGGRDPRGLFTHREMLLQVSRVTEGEPPLARCIAWKKLSSWVAYRNKRSKPKAMSSWAILKNNSHNGVYCEKCKHR-22A
 IRTA1 (82) LYRCCAGCPRENPAVRLFSSTSLLOAPYSVF-EGDMLDRCIRRREREKTPAKVTWNGNILEHSSEKWDILIPZASNNNGVYRIQYGENDVREN
 IRTA2 (82) EVRCCAGCPLESPPVHMFSSASLLOAPLSVF-EGDSNVRCGEKAAVTUNVATK-MNNVLPKKEDEHHPAAKKNQKQVRCVTKYKESCCPVSSN

FCGR1A (172) CKHR--KTSAGSSTVKLEPAPVIVASVMSLKEGNLVTSCGKLLQPLGLQTPSPHMGSLW-RQNVSEZOLIVTRPDGIVWPAVIEDGN
 IRTA1 (171) GENDMFRSNFKIKLOLHHPLEKADQO-TEGNSNMSCGQIPEDPTVIRNTPRIGEVLSDSITYELQVPTVRENKYSWCAETIRAN
 IRTA2 (170) KSSCPSSNTTKIQVOPPTRPVIRASSFOE-SSNPVTLAQVQISLESIMVPIREREREDQIRGLSSILHNFOIAMSKDGEFVKKANVPHS

FCGR1A (269) YKSHHEDEROMLGOPTDWWFHLGYLAVAMFVNIVWVIRKEERKKKDDISLGHKKVTSLODRHFEELKQOE-KEEQLOQEAHH
 IRTA1 (270) GHHEHSIQIHQRIPVGVG-LEQHSSEGAVECEVVMVAEAGGDTASWREDQESLARKQGLRALLEPAGQSHG-CYVPAINSY-
 IRTA2 (269) ASDMERSWLOVG-IPASHNV-ITLSDEKALNFECTKRVTHGCTQDSTRTHYRTHEGV--PIRHRVECEKASISFETTENEC-NVYCAADMGCA

ITAM: E E E I I I
 DXXXXXXX--DXX--YXXLXXXXXXX--YXXL

IRTA1: ESSHISICPAQVHQLQSLYVDVHPKKG-DLVYSEIQTTTLGEEEEEAANTSRTLLEDKDVSVVYSEV
 PECAM: DNKEPLNSDVQYXTEVQVSSAEWSHK-----DLGKKDTEVYSEV
 IRTA2C: DSDSQ---EPTXHNVPAAWEELQPVYT-----NANPRGENVYSEV
 BGP1: ASDQR---DLTEHKPSPSVNHTQDHSN-----DPPKNMNEVTYSTL

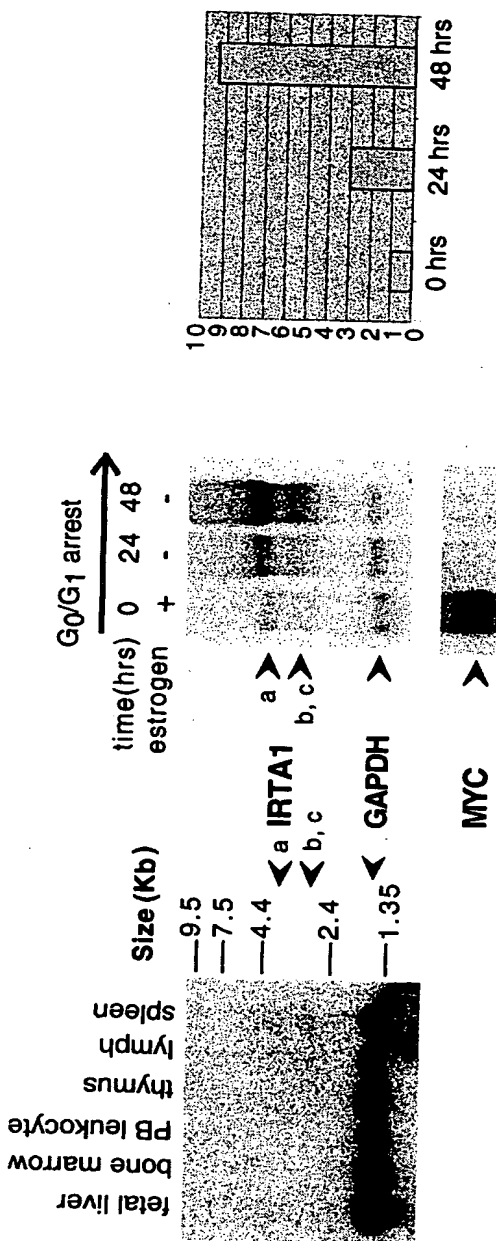
ITIM: SXXXXL SXXXXL SXXXXL
 V V V
 L L L
 I I I

X⁽³⁴⁾ IYSEVK
 X⁽³¹⁾ IYSEVK

FIG. 10B

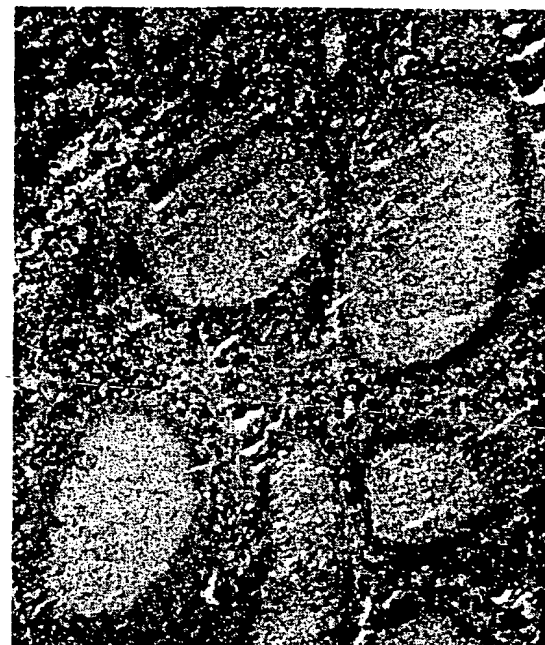
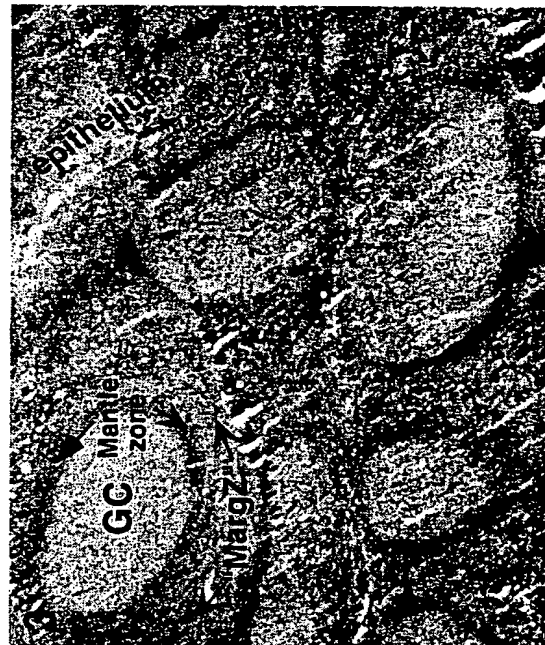
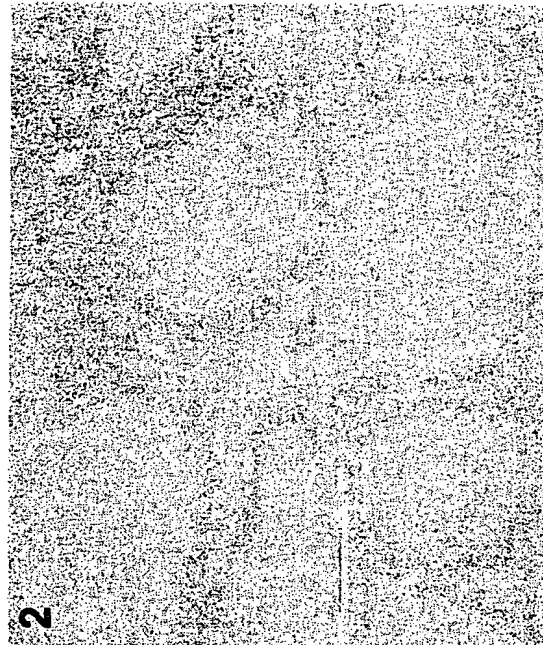
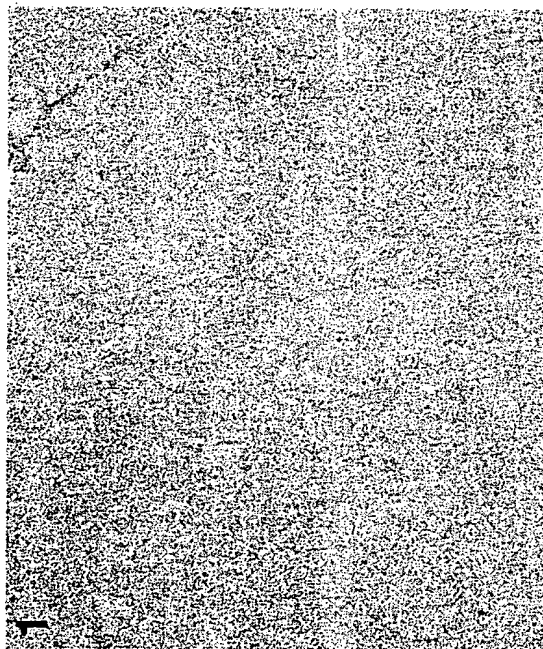
FIGURE 11A

11A



11B1-4

FIGURE 11B1-B4



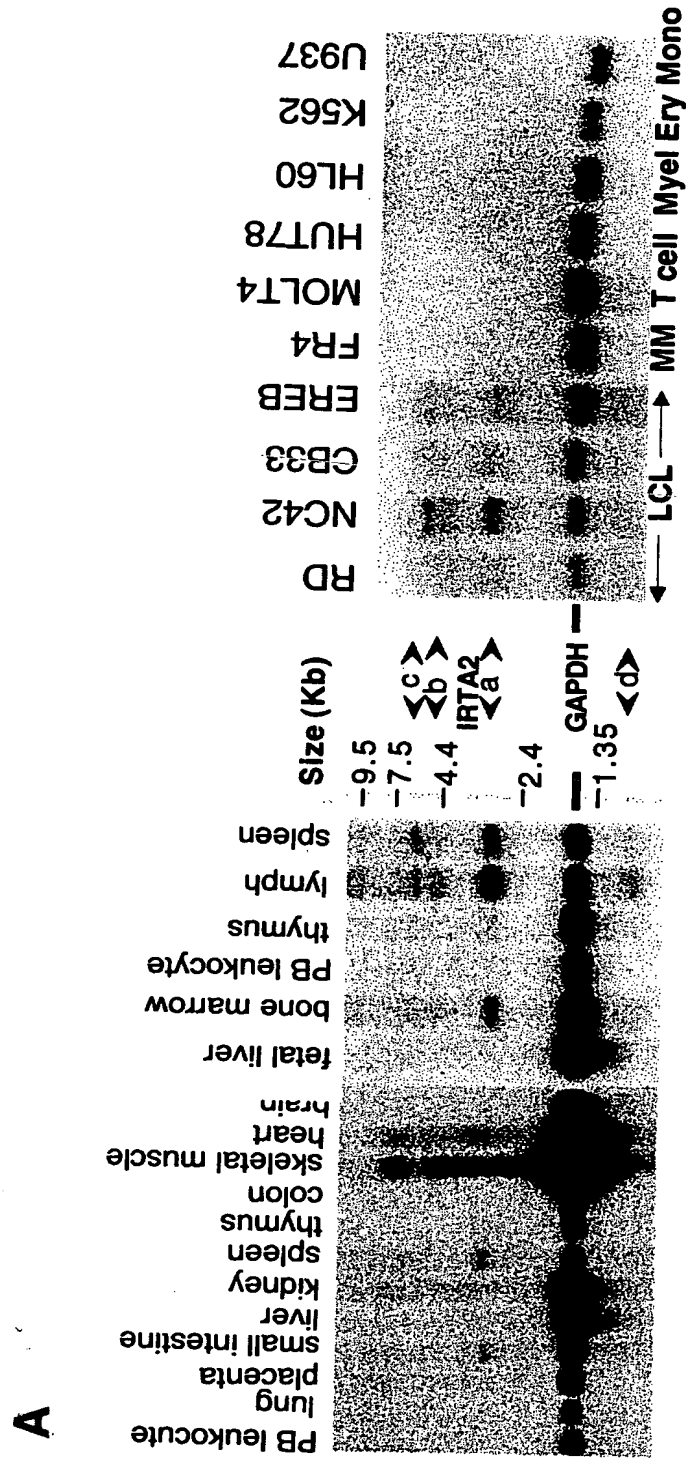
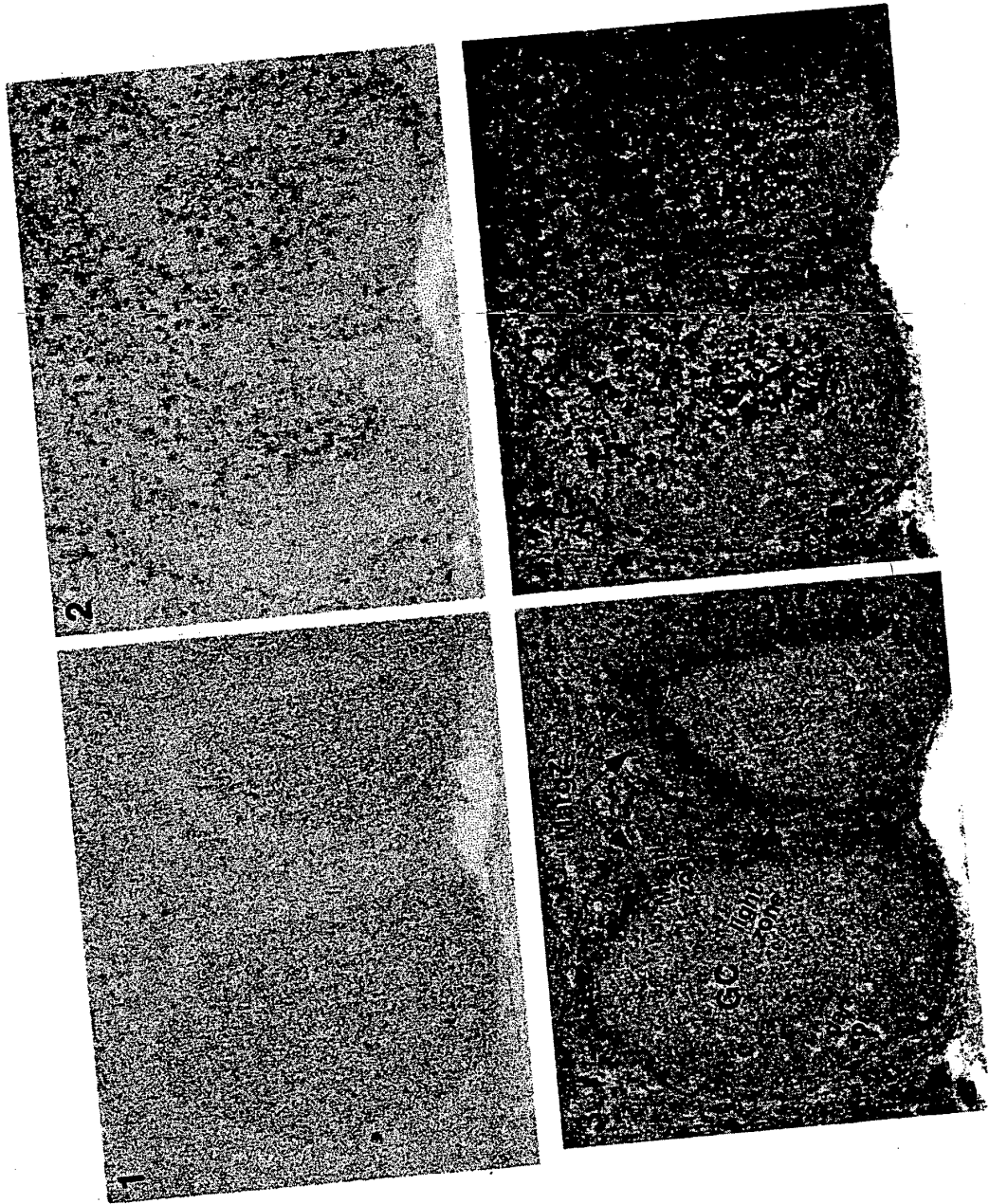


FIGURE 12A.

SECRET
GROUP 1
EXCLUDED FROM AUTOMATIC DOWNGRADING AND DECLASSIFICATION

FIGURE 12B1-B4



B

[illegible]

FIGURE 14

FIG.14A

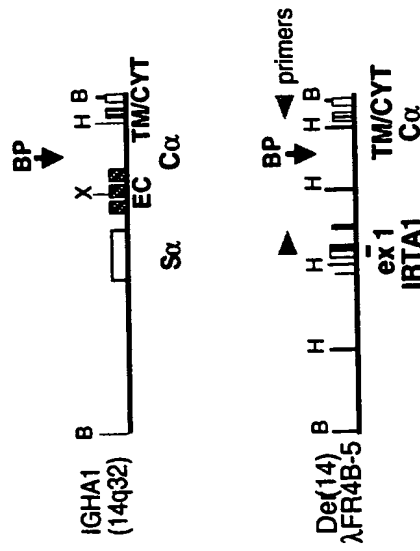


FIG.14C

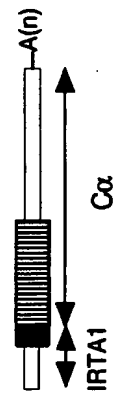


FIG.14B

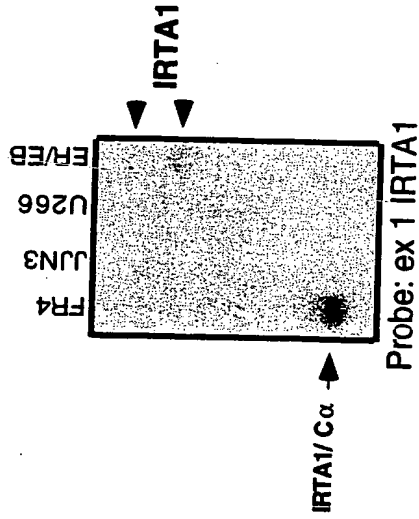


FIG.14D

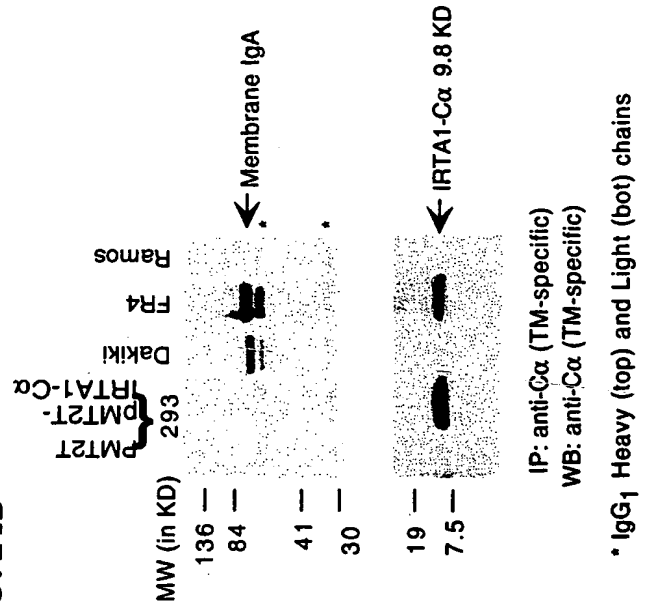


FIGURE 15

FIG.15A

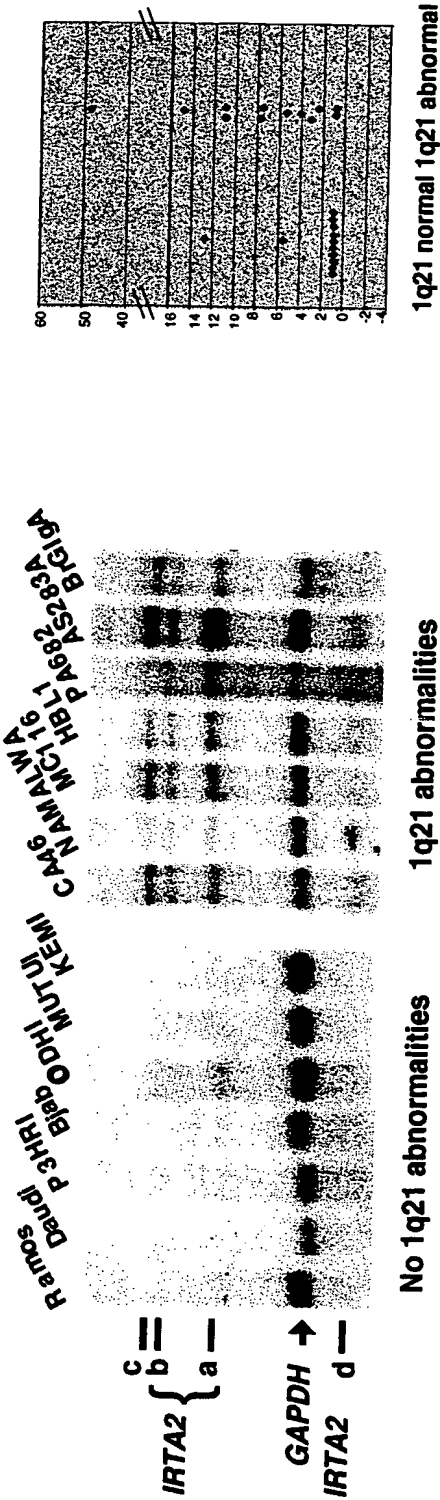
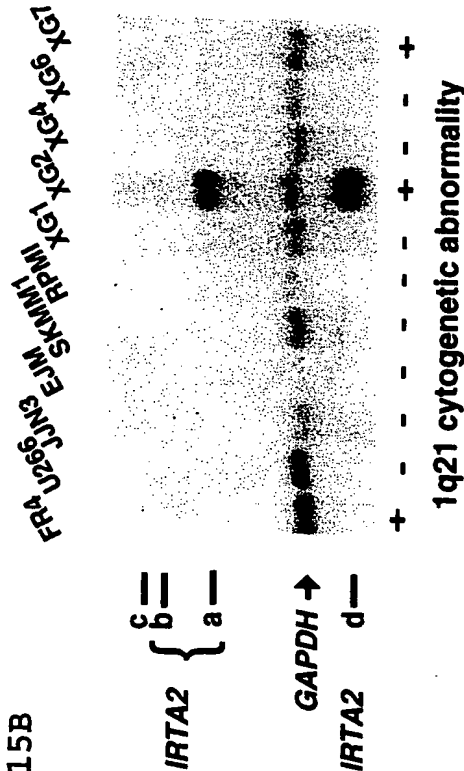


FIG.15B



Cell line	IRTA2
Burkitt Lymphoma	
Normal 1q21	2/12
Abnormal 1q21	10/12
Multiple Myeloma	
Normal 1q21	0/7
Abnormal 1q21	1/3

Summary of IRTA2 expression

FIGURE 16-1~16-4
IRTA1 expression in normal lymphoid tissue



FIGURE 17

IRTA1 expression in a stomach Mucosa-Associated-Lymphoid/Tissue B cell lymphoma

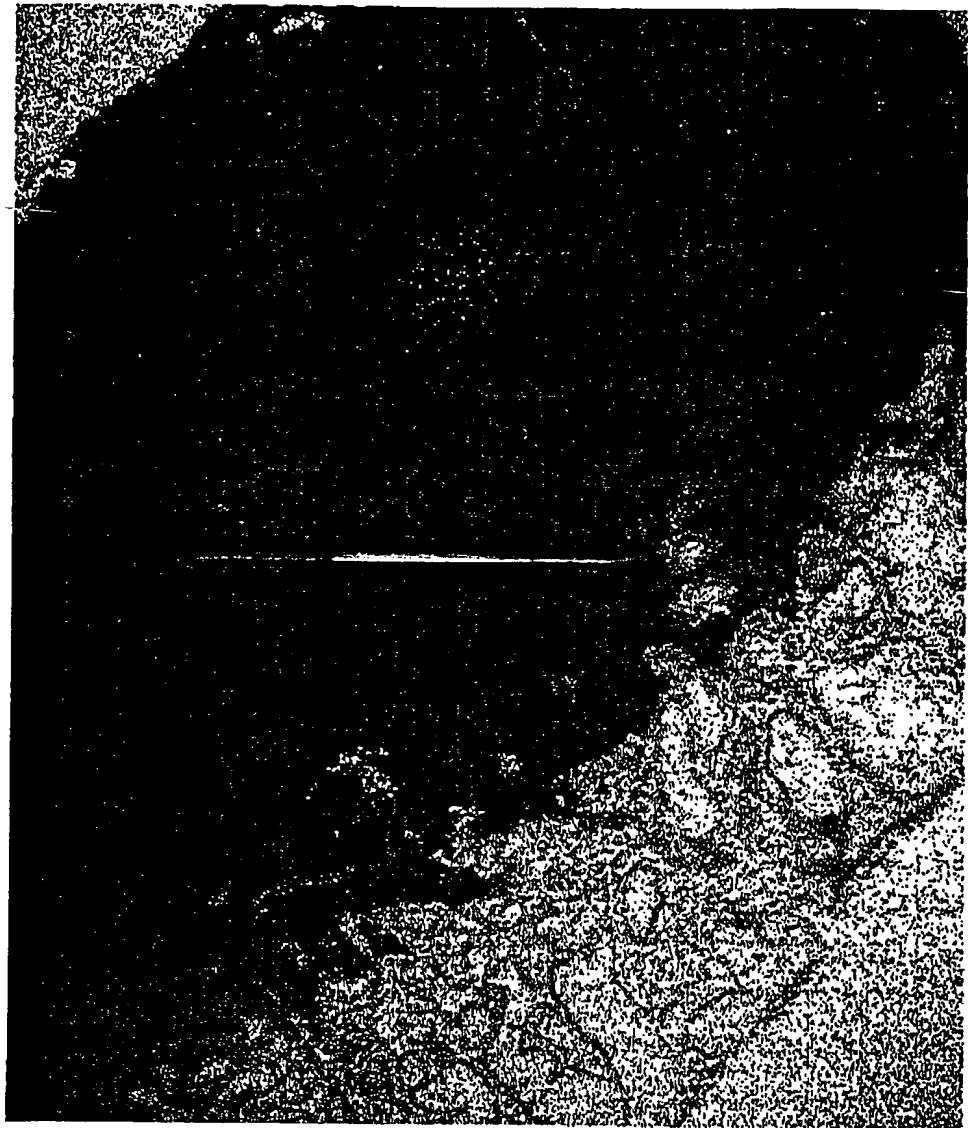


FIGURE 18A

1 CTCAATCAGCTTTATGCGAGAGAAGAAGCTTACTGAGCTCACTGCTGGTGTAGGCAAGTGCTGCTTTGGCAA
 78 TCTGGGCTGACCTGGCTTGTCTCCTCAGAACTCCTTCTCCAACCTGGAGCAGGCTTCCATGCTGCTGGGCGTCC
 L L A F A P V C G Q S A A A H K P V I S V H P P W T 32
 155 TTGCTGGCCTTTGCTCCAGTCTGTGGACAATCTGCAGCTGCACACAAACCTGTGATTTCCGTCCATCCTCCATGGAC
 T F F K G E R V T L T C N G F Q F Y A T E K T T W Y 58
 232 CACATTCTTCAAAGGAGAGAGAGTGAAGTCTGACTTGAATGGATTTCAGTTCTATGCAACAGAGAAAACAACATGGT
 H R H Y W G E K L T L T P G N T L E V R E S G L Y 83
 309 ATCATCGGCACTACTGGGAGAAAAGTTGACCTGACCCAGGAAACACCTCGAGGTTCCGGGAATCTGGACTGTAC
 R C Q A R G S P R S N P V R L L F S S D S L I L Q A 109
 386 AGATGCCAGGCCCGGGTCCCCACGAAGTAACCTGTGCGCTGCTCTTTCTTCAGACTCCTTAATCTGCAGGC
 P Y S V F E G D T L V L R C H R R R K E K L T A V K 135
 463 ACCATATTCTGTGTTTGAAGGTGACACATTGGTTCTGAGATGCCACAGAAGAAGGAAAGAAATGACTGCTGTGA
 Y T W N G S I S N K S W D L L I P Q A S S N 160
 540 AATATACTTGAATGGAACATTCTTTCCATTCTAATAAAGCTGGGATCTTCTTATCCCACAGCAAGTTCAAAT
 N N G N Y R C I G Y G D E N D V F R S N F K I K I 186
 617 AACAATGGCAATTATCGATGCATTGGATATGGAGATGAGAATGATGATTTAGATCAAATTTCAAATTAATAAAT
 Q E L F P H P E L K A T D S Q P T E G N S V C 212
 694 TCAAGAATATTTCCACATCCAGAGCTGAAAGCTACAGACTCTCAGCCTACAGAGGGGAATTCGTAAACCTGAGCT
 E T Q L P P E R S D T P L H F N F R D G E V I L 237
 771 GTGAAACACAGCTTCTCCAGAGCGGTGAGACACCCCACTTCACTTCACTTCTCAGAGATGGCGAGGTCATCTG
 S D W S T Y P E L Q L P T V W R E N S G S Y W C G A 263
 848 TCAGACTGGAGCACGTACCCGAACTCCAGCTCCCAACCGTCTGGAGAGAAAACCTCAGGATCCTATTGGTGTGGTGC
 E T V R G N I H K H S P S L Q I H V Q R I P V S G V 289
 925 TGAAACAGTGAGGGGTAAATCCACAAGCACAGTCCCTCGCTACAGATCCATGTCAGCGGATCCCTGTGTCTGGGG
 L L E T Q P S G G A V E G E M L V L V C S V A E 314
 1002 TGCTCCTGGAGACCCAGCCCTCAGGGGGCCAGGCTGTTGAAGGGAGATGCTGGTCTTGTCTGCTCCGTGAGCTGAA
 G T G D T T F S W H R E D M Q E S L G R K T Q R S L 340
 1079 GGCACAGGGGATACCACATTCTCTGGCACCAGAGGACATGCAGGAGAGTCTGGGGAGGAAAACCTCAGCGTTCCCT
 G A E L E L P A I R Q S H A G G Y Y C T A D N S Y G 366
 1156 GAGAGCAGAGCTGGAGCTCCCTGCCATCAGACAGGCCATGCAGGGGATACTACTGTACAGCAGACAACAGCTACG
 P V Q S M V L V R E T P G N R D G L V A A G 391
 1233 GCCCTGTCCAGAGCATGGTGAATGTCACTGTGAGAGAGACCCAGGCAACAGAGATGGCCTTGTGCGCGCGGGA
 A T G G L L S A L L L A V A L L F H C W R R R K S G 417
 1310 GCCATGGAGGGCTGCTCAGTGTCTTCTCCTGGCTGTGGCCTGCTGTTCACTGCTGGCGTCGGAGGAAGTCAGG
 V G F L G D E T R L P P A P G P G E S S H S I C P A 443
 1387 AGTTGGTTTCTTGGGAGACGAAACCAGGCTCCCTCCCGCTCCAGGCCAGGAGATCCTCCCATTTCCATCTGCCCTG
 Q V E L Q S L Y V D V H P K K G D L V Y S E I Q T 468
 1464 CCCAGGTGGAGCTTCACTGCTTGTATGTGATGTACACCCAAAAAGGAGATTGGTATCTCTGAGATCCAGACT
 T Q L G E E E E A N T S R T L L E D K D V S V V Y S 494
 1541 ACTCAGCTGGGAGAAGAAGAGGAAGCTAATACCTCCAGGACACTTCTAGAGGATAAGGATGTCTCAGTTGTCTACTC
 E V K T Q H P D N S A G K I S S K D E E S * 515
 1618 TGAGGTAAGACACAACACCCAGATAACTCAGCTGGAAGATCAGCTCTAAGGATGAAGAAAGTTAAGAGAATGAAA
 1695 AGTTACGGGAACGTCCTACTCATGTGATTTCTCCCTTGTCCAAGTCCCAGGCCAGTGCAGTCTTGGCGCACCTG
 1772 GAATGATCAACTCATTCCAGCTTCTAATTCTTCTCATGATATGCATTCACTCCAGGAATACTCATTGCTCTACT
 1849 CTGATGTTGGGATGGAATGGCCTCTGAAAGACTTCACTAAAATGACCAGGATCCACAGTTAAGAGAAGACCCTGTAG
 1926 TATTTGCTGTGGCCTGACCTAATGCATTCCCTAGGGTCTGCTTTAGAGAAGGGGATAAAGAGAGAGAAGGACTGT
 2003 TATGAAAAACAGAAGCACAAATTTGGTGAATTTGGGATTGTCAGAGATGAAAAAGACTGGGTGACCTGGATCTCTGC
 2080 TTAATACATCTACAACCATTTGTCTCACTGGAGACTCACTTGCATCAGTTTGTTTAACTGTGAGTGGCTGCACAGGCA
 2157 CTGTGCAAAACAATGAAAAGCCCTTCACTTCTGCCTGCACAGCTTACACTGTGAGGATTCAGTTGCAGATTAAAGAA
 2234 CCCATCTGGAATGGTTTACAGAGAGAGGAATTTAAAGAGGACATCAGAAGAGCTGGAGATGCAAGCTCTAGGCTGC
 2311 GCTTCCAAAAGCAAATGATAATTATGTTAATGTCAATTAGTGACAAAGATTGCAACATTAGAGAAAAGAGACACAAA
 2388 TATAAAATTAATAAAGTAACTACCAACTCTCCAAACTAAATTTGAACCTAAATATTAGTATAAACTCATAATAA
 • CTCTGCCTTTAAATAAAAAAAAAAAAAAAAAAAAAA

IRTA1 cDNA and protein sequence

FIGURE 18B-1

IRTA2A
 IRTA2C
 IRTA2B

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1  CCGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTGGAAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTG
    M L L W V I L L V L A P V S G Q F A R T P R
81  GTGGTCCAGGTCTTCATGCTGCTGTGGGTGATATTACTGGTCTGGCTCCTGTCAGTGGACAGTTTGAAGGACACCCAG
    P I I F L Q P P W T T V F Q G E R V T L T C K G F R F
161  GCCCATTATTTTCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCTCAGTTGCAAGGGATTTTCGCT
    Y S P Q K T K W Y H R Y L G K E I L R E T P D N I L
241  TCTACTCACCACAGAAAACAAATGGTACCATCGGTACCTTGGGAAAGAAATACTAAGAGAAACCCAGACAATATCCTT
    E V Q E S G E Y R C Q A Q G S P L S S P V H L D F S S
321  GAGGTTCAAGAACTGAGAGAGTACAGATGCCAGGCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTCTTC
    A S L I L Q A P L S V F E G D S V V L R C R A K A E V
401  AGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTGAAGGAGACTCTGTGGTTCTGAGGTGCCGGGCAAGGCCGAAG
    T L S P E K A L N F E G T K V T L H C E T Q E D S L
481  TAACACTGATATACTATTACAGAATGATAATGTCCTGGCATTCTTAATAAAGAACTGACTTCCATATTCCTCAT
    A C L K D N G A Y R C T G Y K E S C C P V S S N T V K
561  GCATGTCTCAAGGACAATGGTGCATATCGCTGTACTGGATATAAGGAAAGTTGTTGCCCTTTTCTTCCAATACAGTCAA
    I Q V Q E P F T R P V L R A S S F Q P I S G N P V T L
641  AATCCAAGTCCAAGAGCCATTACACGTCCAGTCTGAGAGCCAGCTCCTTCCAGCCCATCAGCGGGAACCCAGTGACCC
    T C E T Q L S L E R S D V P L R F R F F R D D Q T L
721  TGACCTGTGAGACCCAGCTCTCTCTAGAGAGGTGAGATGTCCCGCTCCGCTTCTTTCAGAGATGACCAGACCCCTG
    G L G W S L S P N F Q I T A M W S K D S G F Y W C K A
801  GGATTAGCTGGAGTCTCTCCCGAATTCCAGATTACTGCCATGTGGAGTAAAGATTACAGGTTCTACTGGTGAAGGC
    A T M P H S V I S D S P R S W I Q V Q I P A S H P V L
881  AGCAACAATGCCTCACAGCGTATATCTGACAGCCGAGATCTGGATACAGGTGCAGATCCCTGCATCTCATCCTGTCC
    T L S P E K A L N F E G T K V T L H C E T Q E D S L
961  TCACTCTCAGCCCTGAAAAGGCTCTGAATTTTGGGGAACCAAGGTGACACTTCACTGTGAAACCCAGGAAGATTCTCTG
    R T L Y R F Y H E G V P L R H K S V R C E R G A S I S
1041  CGCACTTGTACAGGTTTATCATGAGGTTGTCCTGTCCTGTCCTGTCCTGAGGACCTGATTTTGGAGGAGCC
    F S L T T E N S G N Y C T A D N G L G A K P S K A V
1121  CTTCTCACTGACTACAGAAATTCAGGGAATCTACTGCACAGCTGACAATGGCCTTGGCGCCAAGCCAGTAAGGCTG
    S L S V T V P V S H P V L S P E D L I F E G A
1201  TGAGCTCTCAGTCACTGTTCCCGTGTCTCATCTGTCCTGTCCTGTCCTGAGGACCTGATTTTGGAGGAGCC
    K V T L H C E A Q R G S L P I L Y Q F H H E D A A L E
1281  AAGGTGACACTTCACTGTGAAGCCAGAGAGGTTCACTCCCATCCTGTACCAGTTTTCATCATGAGGATGCTGCCCTGGA
    R R S A N S A G G V A I S F S L T A E H S G N Y Y C T
1361  GCGTAGGTGCGCCAACCTCTGCAGGAGGAGTGGCCATCAGCTTCTCTGACTGCAGAGCACTTCAAGGAACTACTGCA
    A D N G F G P Q R S K A V S L S I T V P V S H P V L
1441  CAGCTGACAATGGCTTTGGCCCCAGCGCAGTAAGCGGTGAGCCTCTCCATCACTGTCCCTGTGTCTCATCTGTCCTC
    T L S S A E A L T F E G A T V T L H C E V Q R G S P Q
1521  ACCCTCAGTCTGTGAGGCGCTGACTTTTGAAGGAGCCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCCA
    I L Y Q F Y H E D M P L W S S S T P S V G R V S F S F
1601  AATCTATACAGTTTATCATGAGGACATGCCCTGTGGAGCAGCTCAACACCCCTCTGTGGGAAGAGTGTCTCTCAGCT
    S L T E G H S G N Y Y C T A D N G F G P Q R S E V V
1681  TCTCTGACTGAAGGACATTACAGGAATTACTACTGCACAGCTGACAATGGCTTTGGTCCCGAGCGCAGTGAAGTGGTG
    S L F V T V P V S R P I L T L R V P R A Q A V V G D L
2A,2C1761  AGCCTTTTGTCACTGTTCCAGTGTCTCGCCCCATCTCACCTCAGGGTCCCAGGGCCAGGCTGTGGTGGGGGACCT
    G K C W V L A S H P P L A E F S L T H S F K
2B 1761  -----GGTAAGTGCTGGGTTCTTGCCAGTACCCACCCCTGGCTGAGTTCTCTCACCCATTCTTTAA
    L E L H C E A P R G S P P I L Y W F Y H E D V T L G S
2A,2C1841  GCTGGAGCTTCACTGTGAGGCCCCGAGAGGCTCTCCCCAATCCTGTACTGGTTTATCATGAGGATGTACCCTGGGGA
    N L F A L S S F L P * stop
2B 1841  AAATCTGTTTGCAGTGTCCAGTTTCTCCCTAATCAACTTAATCCCCTTCTTGCTTCTCTCAACTAAGTGGG
    S S A P S G G E A S F L T A E H S G C E
2A,2C1921  GCAGCTCAGCCCCCTCTGAGGAGAAGCTTCTTCAACCTCTCTGACTGCAGAACATTCTGGAACCTACTCATGTGAG
    GTTTCCGTACTCATAAGTCTCGGCTCAGCCAGACCCCTAAACAGCTCAGTAGATTCCCGAGCTTTTACCAATGAATT
2A,2C2001  A N N G L V A Q H S D T I S L S V I V P V S R P I L T
2B 2001  GCCAACAAATGGCCTAGTGGCCAGCAGCAGTACACAATATCACTCAGTGTATAGTTCAGTATCTCGTCCCATCCTCAC
    TATTATTGTATTTTCTCTCATTTCTGTATGTTCCAACAGTACGCCAATTTTCTTGATGCACGGAGCGTGTCTACT
    F R A P R A Q A V V G D L L E L H C E A L R G S S P I
2A,2C2081  CTTCAGGCTCCAGGCCAGGCTGTGGTGGGGACCTGTGGAGCTTCACTGTGAGGCCCTGAGAGGCTCCTCCCA
    TCTCTACTGACATTTACATATTAACCTAGCTACAAGCACAGCTTATAGATAAATATTGGTCAAGACCTTAAATTCTCCA
  
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FIGURE 18B-2

2A, 2C2161 TCCTGTACTGGTTTATCATGAAGATGTACACCTGGTGAAGATCTCAGCCCCCTCTGGAGGAGGGGCTCTTCAACCTC
2B 2161 AAGGATTTCGAATCTTATGGTAGATTGGGAGAAAGCTGCTGGTGAACAAAGGGGAAATGGCTCCCTAGGAACCAACTCC

2A, 2C2241 L T T E H S G I Y S C E A D N G L E A Q R S E M V T
2B 2241 TCTCTGACTACAGAACATTTCTGGAATCTACTCTGTGAGGCAGACAAATGGTCTGGAGGCCAGCGCAGTGAAGTGGTAC
TCAAACCTCTGGAGTTTATGATCCCTGTTTCTTAACTGCTAAAATCAGTATCATTTTATTGATTATTTTAAAAA

2C 2321 L K V A V P V S R P V L T L R A P G T H A A V G D L L
2B 2321 ACTGAAAGTTGCAGTTCCGGTGTCTGCGCCGGTCTCACCTCAGGGCTCCGGGACCCATGCTGCGGTGGGGACCTGC
-----G E W A L P T S S T S E N *
-----GGTGAGTGGGCTGCCCACCAGCAGACATCTGAGAATGACTGTGCTGTCTCTCCCTGCAGCTGA
ACTATTGTTGAAGTATGACATACATTCAAGAAACGTGTGCAAAATGTATGTGTACGATTGGTGTCTTTTAGGAGCTAA

2C 2401 E L H C E A L R G S P L I L Y R F F H E D V T L G
2A 2401 TGGAGCTTCACTGTGAGGCCCTGAGAGGCTCTCCCTGATCTGTACCGTCTTTTTCATGAGGATGTACCCCTAGGAAT
2B 2401 AAATGGAGCCACAGAGCTCTCAGGGCTGTTGCTTGTGTGGCATCCAGCACACTCTCTGCTGCAAGACCTCCCTGTG
GTTGCTTCTGTTTTTACTTGAATCTTTGTTTATAGAACTGGGGAAAGTTTACTTTCTTTTCAGAGAAGCCAAATGGTA

2C 2481 S P S G G A S L L T A E H S G C E A D
2A 2481 AGGTCGTCCCTCTGGAGGAGCGTCTTAACTCTCTCTGACTGCAGAGCACTCTGGAATCTCTCTGTGAGGCCGA
2B 2481 AAAGTCTCGGATCTTTGTTGATGTTCCAGGAATCTGATGTTTCCAGCAGCTCTTCTGAAGATGATCAAGACCTC
TGATAGAAAAATCTTGAGCTGATGTGTGACATGCCCCAGCATAACTGTTGAGTAAAGAGGTTATTTTAAATGT

2C 2561 N G L G A Q R S E T V T L Y I T G L T A G P F A
2A 2561 CAATGGCTCGGGGGCCAGCGCAGTGCAGAGTACACTTTATATCACAGGGCTGACCGGAACAGAAAGTGGCCCTTTG
2B 2561 ACTAAAAATGCAATAAGACTTTTTAGAACATAAACTATATTCTGAAGTAAATATTACATGAAATGAAACCAAGA
GAATGTTCTGAGACTCTCCAAAGTCAGAGCCAAATCTACTAGGAAGCTCTAGACTTCACTCATTCTGCATCCATTAC

2C 2641 T G V A G G L L L S I A G L A A G A L L L Y C W L S R
2A 2641 CCACAGGAGTCCCGGGGGCTGCTCAGCATAGCAGCCTTGCTGCGGGGGCATGCTGCTCTACTGCTGGCTCTCGAGA
2B 2641 ATTCTGAGCATATGTTTCTCTGCCGTAGAAAGGATTAAGCTGTTTCTGTCGGGATCTTCTCTCATTGACTTCTAAGA
TATCTTTTATCCATGTTTCTTCTTCTCATATTGAGCAGCATCTTAAGCTCTTTATTTTCTGTTTCTGACTGTCA

2C 2721 K A G R K P A S D P A R S P S D S D S Q E P T Y H N V
2A 2721 AAAGCAGGGAGAAAGCTGCTCTGACCCCGCCAGGAGCCCTCAGACTCGGACTCCCAAGAGCCCACTATCAAGT
2B 2721 GCCTCTGCTTGTAGTCTCTTTCATTACTGGGATGTAATGTTCTCTTACATTCCACATTAAAACTATGTTAACA
CCCTTAATGCCAGTAGAATGTAAGCTTCATGAGAACAGAACTGCATCCATCTTGCTCTCAACATCCCTGTGCTACT

2C 2801 P A W E E L Q P V Y T N A N P R G E N V V Y S E V R I
2A 2801 ACCAGCTGGGAAGAGCTGCAACAGTGTACACTAATGCAAACTCTAGAGGAGAAAAATGTGGTTTACTCAGAAGTACGA
2B 2801 CAGTGTTTGGCACACAGTAGTCTCAGTCAACATTTGTAATTTAGTGGACAGATGATATGACAAGATGATAAGAGGGGA

2C 2881 I Q E K K K H A V A S D P R H L R N K G S P I I Y S
2B 2881 TCATCAAGAGAAAAAGAAACATGCAAGTGGCTCTGACCCAGGCATCTCAGGAACAGGGTTCCCTATCATCTACTCT
TTTAAAAAATCATCTAGCAAAGCCCAAGAGGAAAAAACAAGCTATTTAGAAATGAAATACCAATTTGAAGCAGTA

2C 2961 E V K V A S T P V S G S L F L A S S A P H R * stop
2B 2961 GAAATTAAGGTGGCGTCAACCCCGTTCGGGATCCCTGTTCTTGCTCTCCTCAGCTCCTCAGATGAGTCCACAGT
AGAATAGATTGGATATCTTTGAAAACCATTAATTGAATGAAGAACCAATTTAGAAAAAATACAGAATGCAAGTAGAA

2C 3041 TCTCCAATGCTGTTTACGCTCTGCACCCCAAGTTCCCTTGGGGGAGAAGCAGCATTTGAAGTGGGAAGATTTAGGCT
2B 3041 AGATACAGAAATAAGGCCAAAAGTTATAATATGAAATCAGACCAATGGATTGTCTGTATCCAGTTATGTGGATAATTAA

2C 3121 GCCCCAGACCATATCTACTGGCTTTGTTTTCATGTCTCTCAGTCTGACCAGAATGCAGGGCCCTGCTGGACTG
2B 3121 AATGGAGACCCCTCAGAAAAATTGAACCGAAGAGTAAATGAAACTCAAAATGTAGTAGAAATGTTGGGAAGTAAAGAA

2C 3201 TCACCTGTTTCCAGTTAAAGCCCTGACTGGCAGGTTTTTAAATCCAGTGGCAAGGTGCTCCCACTCCAGGGCCAGCAC
2B 3201 ACTTGAATATGTAGATCAGAACATATATGTTGATGACGTTATTGACTTTGAGGTTAAAAATATATATATGTTGCTATGAT

2C 3281 ATCTCCTGGATTCTTGTAGTGGGCTCAGCTGTGGTTGCTGTTCTGAGTACTGCTCTCATCACCCCCCAGAGGGGTC
2B 3281 TATGGGAAAAAAGCAGTCGTCTCAGAAAGAAAAACATAAGTTAGTCTTAGACTTTGCACTGCACTCAGTACCAAGAG

3361 TTACCAACAAAGGGAGAGTGGGCTTCAGGAGATGCCGGGCTGGCTTAACAGCTCAGGTGCTCTAACTCCGACACAG
3441 AGTTCCTGCTTTGGGTGGATGCAATTTCTCAATTTGTCATCAGCCTGGTGGGGCTACTGCACTGTGCTGCCAAATGGGACAG
3521 CACACAGCTGTGCATAGGACATGTGATGGGTCTCCCCAGGGGGCTGCTATTTACACTCTCCACCTGTCTCAACT
3601 CTAAGGTGGCCTATGACACCAAGGTAATCTCTCTGCTCATGTGTCTACGTCTACCTGCCCAAGTAAGTGGCTTTCA
3681 TACACCAAGTCCCGAAGTCTTCCATCTTAACAGAAGTAACCCAGCAAGTCAAGGCCAGGAGCCAGGGGTGCAGACA
3761 GAACACATCTGGAACACAGAGGTTGCTCAATTAATTAATGACTGACTGACTGACTGAATGAATGAATGAGGAAGAAAC
3841 TGTGGGTAATCAACTGGCATAAAATCCAGTCACTCCCTAGGAAATCCGGGAGGTATCTGGCTCTCAATGAAGAACCG
3921 GAAGAAAGGAGCTTGGATGAAGAACTGTTGAGGAAAGAGGGCTTCTTCACTTTTATGTGCTGTGGATCACCT
4001 GAGGATCTGTGAAAAATACAGATACTGATTCAGTGGGCTGTGTAGAGCCTGAGACTGCCATTCTACATGTTCCAGGGG

FIGURE 18B-3

4081 ATGCTGATGCTGCTGGCCCTGGGACTGCACTGCATGCATGTGAAGCCCTATAGGTCTCAGCAGAGGCCCATGGAGAGGGA
4161 ATGTGTGGCTCTGGCTGCCAGGGCCCAACTCGGTTTACACGGATCGTGCTGCTCCCTGGCCAGCCTTTGGCCACAGCAC
4241 CACCAGCTGCTGTTGCTGAGAGAGCTTCTTCTGTGACATGTTGGCTTTCATCAGCCACCTGGGAAGCGGAAAGTAGC
4321 TGCCACTATCTTTGTTTCCCACTCAGGCCTCACACTTCCCATGAAAAGGGTGAATGTATATAACCTGAGCCCTCTCC
4401 ATTCAGAGTTGTTCTCCCATCTCTGAGCAATGGGATGTTCTGTTCCGCTTTTATGATATCCATCACATCTTATCTTGATC
4481 TTTGCTCCCACTGGATTGTACAGTGATGACTTTAAGCCCCACGGCCCTGAAATAAAATCCTTCCAAGGGCATTGGAAGC
4561 TCACTCCACCTGAACCATGGCTTTTCTGCTTCCAAGTGTGTCAGGGCCTTGCCAGATAGACAGGGCTGACTCTGCTGCC
4641 CAACCTTTCAAGGAGGAAACCAGACACCTGAGACAGGAGCCTGTATGCAGCCAGTGCAGCCTTGACAGGACAAGGCTG
4721 GAGGCATTTGTCTCATCTACAGATATGCAACTAAAATAGACGTGGAGCAAGAGAAATGCATTCEGACCGAGGCGCTTTT
4801 TTAGGCCTAGTTGAAAGTCAAGAAGGACAGCAGCAAGCATAGGCTCAGGATTAAAGAAAAAATCTGCTCACAGTCTGTT
4881 CTGGAGGTCAATCACCACAAAGCTCACGCCCTATGCAGTTCTGAGAAGGTGGAGGCACAGGCTCAAAAGAGGAAAT
4961 TAGAATTTCTCATTGGGAGAGTAAGGTACCCCTATCCAGAAATGATAACTGCACAGTGGCAGAACAACTCCACCTAAT
5041 GTGGGTGGACCCCATCCAGTCTGTTGAAGGCCTGAATGTAACAAAGGGCTTATTCTTCTCAAGTAAGGGGGAACCT
5121 GCTTTGGGCTGGGACATAAGTTTCTGCTTTCAGACGCAAACTGAAAAATGGCTCTTCTTGGGTCTTGAGCTTGCTGGC
5201 ATATGGACTGAAAGAACTATGCTATTGGATCTCCTGGATCTCAGCTTGCTGACTGCAGATCTTGAGATATGTCAGCCT
5281 CTACAGTCACAAGAGCTAATTCATTCTAATAAACCAATCTTC

FIGURE 18C-1

1 AGTGAAGGGGTTTCCCATATGAAAAATACAGAAAGAATTATTTGAATACTA
52 GCAAATACACAACCTTGATATTTCTAGAGAACCAGGCACAGTCTTGGAGAC
103 ATTACTCCTGAGAGACTGCAGCTGATGGAAGATGAGCCCCAAGTCTTAAAAA
154 ATGTATCACTACCGGGATTGAGATACAAACAGCATTAGGAAGGTCTCATC
205 TGAGTAGCAGCTTCTGCCCCTCTTCTTGGAGATAAGTCGGGCTTTTGGTG
256 AGACAGACTTTCCCAACCTCTGCCCGCCGGTGCCCATGCTTCTGTGGCT
1 M L L W L
307 GCTGCTGCTGATCCTGACTCCTGGAAGAGAACAATCAGGGGTGGCCCCAAA
6 L L L I L T P G R E Q S G V A P K
358 AGCTGTACTTCTCCTCAATCCTCCATGGTCCACAGCCTTCAAAGGAGAAAA
23 A V L L L N P P W S T A F K G E K
409 AGTGGCTCTCATATGCAGCAGCATATCACATTCCCTAGCCCAGGAGACAC
40 V A L I C S S I S H S L A Q G D T
460 ATATTGGTATCAGATGAGAAGTTGTTGAAAAATAACATGACAAGATCCA
57 Y W Y H D E K L L K I K H D K I Q
511 AATTACAGAGCCTGGAAATTACCAATGTAAGACCCGAGGATCCTCCCTCAG
74 I T E P G N Y Q C K T R G S S L S
562 TGATGCCGTGCATGTGGAATTTTCACTGACTGGCTGATCCTGCAGGCTTT
91 D A V H V E F S P D W L I L Q A L
613 ACATCCTGTCTTTGAAGGAGACAATGTCTTCTGAGATGTCAGGGGAAAGA
108 H P V F E G D N V I L R C Q G K D
664 CAACAAAAACACTCATCAAAGGTTTACTACAAGGATGAAAAACAGCTTCC
125 N K N T H Q K V Y Y K D G K Q L P
715 TAATAGTTATAATTTAGAGAAGATCACAGTGAATTCAGTCTCCAGGGATAA
142 N S Y N L E K I T V N S V S R D N
766 TAGCAAAATATCATTGTACTGCTTATAGGAAGTTTACATACTTGACATTGA
159 S K Y H C T A Y R K F Y I L D I E
817 AGTAACTTCAAAACCCCTAAATATCCAAGTTCAAGAGCTGTTTCTACATCC
176 V T S K P L N I Q V Q E L F L H P
868 TGTGCTGAGAGCCAGCTCTTCCACGCCCATAGAGGGGAGTCCCATGACCCT
193 V L R A S S S T P I E G S P M T L
919 GACCTGTGAGACCCAGCTCTCTCCACAGAGGCCAGATGTCCAGCTGCAATT
210 T C E T Q L S P Q R P D V Q L Q F
970 CTCCTCTTCAAGATAGCCAGACCCTCGGATTGGGCTGGAGCAGGTCCCC
227 S L F R D S Q T L G L G W S R S P
1021 CAGATCCAGATCCCTGCCATGTGGACTGAAGACTCAGGGTCTTACTGGTG
244 R L Q I P A M W T E D S G S Y W C
1072 TGAGGTGGAGACAGTGACTCACAGCATCAAAAAAGGAGCCTGAGATCTCA
261 E V E T V T H S I K K R S L R S Q
1123 GATACGTGTACAGAGAGTCCCTGTGTCTAATGTGAATCTAGAGATCCGGCC
278 I R V Q R V P V S N V N L E I R P
1174 CACCGGAGGCGAGCTGATTGAAGGAGAAAAATGGTCCTTATTGCTCAGT
295 T G G Q L I E G E N M V L I C S V
1225 AGCCCAGGGTTCAAGGACTGTACATTCTCCTGGCACAAGAAGGAAGAGT
312 A Q G S G T V T F S W H K E G R V
1276 AAGAAGCCTGGGTAGAAAGACCCAGCGTTCCCTGTTGGCAGAGCTAGTG
329 R S L G R K T Q R S L L A E L H V
1327 TCTCACCGTGAAGGAGAGTGATGCAGGGAGATACTACTGTGCAGCTGATAA
346 L T V K E S D A G R Y Y C A A D N
1378 CGTTCACAGCCCCATCCTCAGCACGTGGATTTCAGTACCCGTGAGAATTCC
363 V H S P I L S T W I R V T V R I P
1429 GGTATCTACCCCTGTCTCACCTTCAGGGCTCCCGGGCCCACTGTGGT
380 V S H P V L T F R A P R A H T V V
1480 GGGGACCTGCTGGAGCTTCACTGTGAGTCCCTGAGAGGCTCTCCCCGAT
397 G D L L E L H C E S L R G S P P I
1531 CCTGTACCGATTATCATGAGGATGTACCCCTGGGGAACAGCTCAGCCCC
414 L Y R F Y H E D V T L G N S S A P
1582 CTCTGGAGGAGGAGCCTCCTTCAACCTCTCTCTGACTGCAGAACATTCTGG
431 S G G G A S F N L S L T A E H S G
1633 AAATACTCCTGTGATGCAGACAATGGCCTGGGGGCCAGCACAGTCATGG
448 N Y S C D A D N G L G A Q H S H G
1684 AGTGAGTCTCAGGGTCACAGTTCGGGTGTCTCGCCCCGTCTCACCTCAG
465 V S L R V T V P V S R P V L T L R
1735 GGCTCCCGGGGCCAGGCTGTGGTGGGGGACCTGCTGGAGCTTCACTGTGA
483 A P G A Q A V V G D L L E L H C E
1786 GTCCCTGAGAGGCTCCTTCCCGATCCTGTACTGGTTTATCACGAGATGA
499 S L R G S F P I L Y W F Y H E D D
1837 CACCTTGGGGAACATCTCGGCCACTCTGGAGGAGGGGCATCCTTCAACCT
516 T L G N I S A H S G G G A S F N L
1888 CTCTCTGACTACAGAATCTTGGAACTACTCATGTGAGGCTGACAAATGG
533 S L T T E H S G N Y S C E A D N G

1

1939 CCTGGGGGCCAGCAGCAGTAAAGTGGTGACACTCAATGTACAGGAACCTC
550 L G A Q H S K V V T L N V T G T S
1990 CAGGAACAGAACAGGCCTTACCGCTGCGGGGAATCAGGGGGCTGGTGTCTCAG
567 R N R T G L T A A G I T G L V L S
2041 CATCCTCGTCTTGTCTGCTGCTGCTGCTGCTGATTACGCCAGGGCCCC
584 I L V L A A A A A L L H Y A R A R
2092 AAGGAACAGGAGGACTTCTGCCACTGTGGAACATCTAGTCACAGTCTCTAG
601 R K P G G L S A C T G T S S H S P S
2143 TGAGTGTCTAGGAGCCTTCTCTCGTCCAGGCCTTCCAGGATAGCCCTCAAGA
618 E C Q E P S S S R P S R I D P Q E
2194 GCCCATCTACTCTAAACCACCTAGCCCCAATGGAGCTGGAGCCCATGTACAG
635 P T H S K P L A P M E L E P M Y S
2245 CAATGTAAATCTGGAGATAGCAAGCGGATTTATCTCCAGATCTGGAGCAT
652 N V N P G D S N P I Y S Q I W S I
2296 CCAGCATACAAAAGAAAACCTAGCTAAITGTCCATGATGCATCAAGAGCA
669 Q H T K E N S A N C P M M H Q E H
2347 TGAGGAACCTTACAGTCTCTATTTCAGAACTGAAGAAGCACACCCAGACGA
686 E E L T V L Y S E L K K T H P D D
2398 CTCTGCAGGGGAGGCTAGCAGCAGAGGCGCCCATGAAGAAGATGTGA
703 S A A G E A S S R G R A H E E D D E
2449 AGAAACTATGAGAATGTACCACGTGTATTACTGGCTCAGACCCACTAGCC
720 E N Y E N V P R V L L A S D H
2500 CCTTACCCAGAGTGGCCCCACAGGAACAGCCTGCACCATTTTTTTTCTGT
2551 TCTCTCCAACACACATCATCCATCTCTCCAGACTCTGCCTCTACGAGGC
2602 TGGGCTGCAGGGTATGTGAGGCTGAGCAAAGGCTCGCAATCTCCCTGT
2653 GCCTGATCTGTGTGTTCCCCAGGAAGAGAGCAGGCAGCCTTGAGCAAGCA
2704 CTGTGTTATTTTACAGTGGAGACAGTGGCAAGGCAGGAGGGCCCTCAGC
2755 TCCTAGGGCTTCGAATAGAGGAGGAGAGAAATGGTCTAGCCAGGGTTA
2805 CAAGGGCACAATCATGACCAATTTGATCCAACTGTGATCGAAAGCTGTTAAT
2857 GTGCTCTCTGTATAAACAAATTTGCTCCAAATATTTTGTTTTCCCTTTTGT
2908 GTGGCTGGTAGTGGCATTTGCTGATGTTTTGGTGTATATGCTGTATCCTTGC
2959 TACCATTATTTGGG

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FIGURE 18D-1

1 TGGTGACCAAGAGTACATCTCTTTTCAAATAGCTGGATTAGGTCCTCATGC
19 L W S L L V I F D A V T E Q A D S
103 CGCTGACCCTTGTGGCGCCCTCTTCTGTCTTGAAGGAGACAGCATCGTTC
36 L T L V A P S S V F E G D S I V L
154 TGAATGCCAGGAGAACAGAACTGGAAAATTGAGAAGATGGCTTACCATA
53 K C Q G E Q N W K I Q K M A Y H K
205 AGGATAACAAGAGTTATCTGTTTCAAAAAATTCTCAGATTCTCTTATCC
70 D N K E L S V F K K F S D F L I Q
256 AAAGTGCAGTTTAAAGTGACAGTGGTAATTTCTGTAGTACCAAGGAC
87 S A V L S D S G N Y F C S T K G Q
307 AACTCTTCTCTGGGATAAACTTCAAATATAGTAAAGATAAAAGTCCAAG
104 L F L W D K T S N I V K I K V Q E
358 AGCTCTTCAACGTCCTGTGCTGACTGCCAGCTCTTCCAGCCCATCGAAG
121 L F Q R P V L T A S S F Q P I E G
409 GGGTCCAGTGAGCCTGAAATGTGAGACCCGGCTCTTCCACAGAGGTGG
138 G P V S L K C E T R L S P Q R L D
460 ATGTTCAACTCCAGTTCTGCTTCTCAGAGAAAACAGGTCCCTGGGTGAC
155 V Q L Q F C F F R E N Q V L G S G
511 GCTGGAGCAGCTCTCCGGAGCTCCAGATTTCTGCGGTGTGAGTGAAGACA
172 W S S S P E L Q I S A V W S E D T
562 CAGGGTCTTACTGGTGCAAGGCAGAAACGGTGACTCACAGGATCAGAAAAC
189 G S Y W C K A E T V T H R I R K Q
613 AGAGCCTCCAATCCAGATTACGTGCAGAGAATCCCATCTCTAATGTAA
206 S L Q S Q I H V Q R I P I S N V S
664 GCTTGAGATCCGGGCCCCGGGGGACAGGTGACTGAAGGACAAAACCTGA
223 L E I R A P G G Q V T E G Q K L I
715 TCCTGCTCTGCTCAGTGGCTGGGGTACAGGAATGTACATTCTCCTGGT
240 L L C S V A G G T G N V T F S W Y
766 ACAGAGAGGCCACAGGAACAGTATGGGAAAGAAAACCCAGCGTTCCTGT
257 R E A T G T S M G K K T Q R S L S
817 CAGCAGAGCTGGAGATCCAGCTGTGAAAGAGAGTGATGCCGGCAAATATT
274 A E L E I P A V K E S D A G K Y Y
868 ACTGTAGAGCTGACAACGGCCATGTGCCTATCCAGAGCAAGGTGGTGAATA
291 C R A D N G H V P I Q S K V V N I
919 TCCCTGTGAGAAATCCAGTGTCTCGCCCTGTCTCACCTCAGGTCTCCTG
308 P V R I P V S R P V L T L R S P G
970 GGGCCAGGCTGCAGTGGGGACCTGTGGAGCTTCACTGTGAGGCCCTGA
325 A Q A A V G D L L E L H C E A L R
1021 GAGGCTCTCCCCAATCTGTACCAATTTTATCATGAGGATGTACCCTTG
342 G S P P I L Y Q F Y H E D V T L G
1072 GGAACAGCTCGGCCCTCTGGAGGAGGGCCTCTTCAACTCTCTTTGA
359 N S S A P S G G G A S F N L S L T
1123 CTGCAGAACATTCTGGAATACTCTGTGAGGCCAACACGGCCTGGGG
376 A E H S G N Y S C E A N N G L G A
1174 CCCAGTGCAGTGAGGAGTCCAGTCTCCATCTCAGGACCTGATGGCTATA
393 Q C S E A V P V S I S G P D G Y R
1225 GAAGAGACCTCATGACAGCTGGAGTTCTCTGGGGACTGTTGGTGTCTTG
410 R D L M T A G V L W G L F G V L G
1276 GTTCACTGGTGTGCTTTGCTGTGTATGCCTTGTCCACAAGATATCAG
427 F T G V A L L L Y A L F H K I S G
1327 GAGAAAGTTCTGCCAATAATGAACCCAGAGGGCTTCCAGGCCAAATCCTC
444 E S S A T N E P R G A S R P N P Q
1378 AAGAGTTCACCTATTCAAGCCCAACCCAGACATGGAGGAGCTGCAGCCAG
461 E F T Y S S P T P D M E E L Q P V
1429 TGTATGCAATGTGGGCTCTGTAGATGTGGATGTGGTTTATTCTCAGGTCT
478 Y V N V G S V D V D V V Y S Q V W
1480 GGAGCATGCAGCAGCCAGAAAGCTCAGCAACATCAGGACACTTCTGGAGA
495 S M Q Q P E S S A N I R T L L E N
1531 ACAAGGACTCCCAAGTCATCTACTTCTGTGAAGAAATCATAACACTTG
512 K D S Q V I Y S S V K K S
1582 AGGAATCAGAAGGAAGATCAACAGCAAGGATGGGGCATTAAGACTTG
1633 CTATAAAACCTTATGAAATGCTTGAGGCTTATCACTGCCACAGCAGAA
1684 CTGCTCAGGAGGCACCTCTGTCTTTTGTCTGATGATGTTCTTCT
1735 CCAATATCTCTTTTACCTATCAATATTCTTGAAGCAATCAGTGTG
1786 AACTGTGCAAAATAAATTTCTGCTACCTTCTCTTAAGCAATCAGTGTG
1837 TAAAGATTTGAGGGAAGAATGAATAAGAGATACAAGGTCTCACCTTCTAT
1888 ACTGTGAAGTATGAGAACAGGACTTGATAGTGGTGTATTAACTTATTAT
1939 GTGCTGCTGGATACAGTTTGCTAATATTTTGTGAGAATTTTGCATAATAT

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FIGURE 18D-2

1990 GTTCATTGGGAATATTGGCCTGAAATTTCTTTTCCACTGTGTCTCTGCCA
2041 GAATGTTTGTATCAGGCTGATGCTGGCTTCATAGAATGAGTTAGGCAGGAG
2092 CCCTTCCTCCTTGATTTTTTGGCATAGTTTCAGCAGGATTGGTACCAGTTA
2143 TTCTTTCTGCATCTTGTAAGTTTATTACTAATCAACTTCAGCGCTTGAT
2194 TTTGTGTGGTTGGTAAGTTTCTGTCTCTTCTGGTTCAATCTTGGGAGATTG
2245 ATTGGTCTAGGAGGGTTTCTGTCTCTTCTCCAGATTTCCTTTATGTGCA
2296 TGTGTTCCAGGAATTTAGCCGTTTCTCCAGATTTCCTTTATGTGCA
2347 TCGACTTGAGTGTAACATAACTTATATGCACTGGGAAACCAAAAATCTG
2398 TGTGACTTGCTTTATTGCAAGTATGCATATAGTTGCAAAAATGTGATTTTGA
2449 ACCTGCAATATCACCAAAGTATGCATATAGTTGCAAAAATGTGATTTTGA
2500 CATAGTAAATATGAGTATTTGCAATAAATATGATATTACTTTTGTAAAGTA
2551 TATAGAATAAAATGTAATAATCTATAAAA

FIGURE 18E-1

1 GAGGCATCTCTAGGTACCATCCCTGACCTGGTCCTC
 37 ATGCTGCCGAGGCTGTTGCTGTTGATCTGTGCTCCACTCTGTGAA
 M L P R L L L L I C A P L C E 15
 82 CCTGCCGAGCTGTTTTGATAGCCAGCCCTCCCATCCACAGAG
 P A E L F L I A S P S H P T E 30
 127 GGGAGCCAGTGACCTGACGTGTAAGATGCCCTTTCTACAGAGT
 G S P V T L T C K M P F L Q S 45
 172 TCAGATGCCAGTTCCAGTTCTGCTTTTTCAGAGACACCCGGGCC
 S D A Q F Q F C F F R D T R A 60
 217 TTGGGCCAGGCTGGAGCAGCTCCCCAAGCTCCAGATCGCTGCC
 L G P G W S S S P K L Q I A A 75
 262 ATGTGGAAGAAGACACAGGGTCATACTGGTGCAGGCACAGACA
 M W K E D T G S Y W C E A Q T 90
 307 ATGGCGTCCAAAGTCTTGAGGAGCAGGAGATCCAGATAAATGTG
 M A S K V L R S R R S Q I N V 105
 352 CACAGGGTCCCTGTGCTGATGTGAGCTTGGAGACTCAGCCCCCA
 H R V P V A D V S L E T Q P P
 397 GGAGGACAGGTGATGGAGGGAGACAGGCTGGTCTCATCTGCTCA
 G G Q V M E G D R L V L I C S
 442 GTTGCTATGGGCACAGGAGACATCACCTTCCTTTGGTACAAAGGG
 V A M G T G D I T F L W Y K G
 487 GCTGTAGGTTTAAACCTTCAGTCAAAGACCCAGCGTTCAGTGACA
 A V G L N L Q S K T Q R S L T
 532 GCAGAGTATGAGATTCCCTTCAGTGAGGAGAGTGATGCTGAGCAA
 A E Y E I P S V R E S D A E Q
 577 TATTACTGTGTAGCTGAAAATGGCTATGGTCCCAGCCCCAGTGGG
 Y Y C V A E N G Y G P S P S G
 622 CTGGTGAGCATCACTGTGAGAATCCCGGTGTCTCGCCCAATCCTC
 L V S I T V R I P V S R P I L 210
 667 ATGCTCAGGGCTCCCAGGGCCAGGCTGCAGTGGAGGATGTGCTG
 M L R A P R A Q A A V E D V L
 712 GAGCTTCACTGTGAGGCCCTGAGAGGCTCTCCTCCAATCCTGTAC
 E L H C E A L R G S P P I L Y
 757 TGGTTTTATCACGAGGATATCACCTTGGGGAGCAGGTGCGCCCCC
 W F Y H E D I T L G S R S A P
 802 TCTGGAGGAGGAGCCTCCTCAACCTTCCCTGACTGAAGAACAT
 S G G G A S F N L S L T E E H
 847 TCTGGAAACTACTCCTGTGAGGCCAACAATGGCCTGGGGGCCAG
 S G N Y S C E A N N G L G A Q
 892 CGCAGTGAGGCGGTGACACTCAACTTCACAGTGCCCTACTGGGGCC
 R S E A V T L N F T V P T G A
 937 AGAAGCAATCATCTTACCTCAGGAGTCATTGAGGGGCTGCTCAGC
 R S N H L T S G V I E G L L S 315
 982 ACCCTTGGTCCAGCCACCGTGGCCTTATTATTGCTACGGCCTC
 T L G P A T V A L L F C Y G L
 1027 AAAAGAAAAATAGGAAGACGTTTCAGCCAGGGATCCACTCAGGAGC
 K R K I G R R S A R D P L R S
 1072 CTTCCCGCCCTCTACCCCAAGAGTTTACCTACCTCAACTCACCT
 L P S P L P Q E F T Y L N S P
 1117 ACCCCAGGGCAGCTACAGCCTATATATGAAAATGTGAATGTTGTA
 T P G Q L Q P I Y E N V N V V
 1162 AGTGGGGATGAGGTTTATTCACTGGCGTACTATAACCAGCCGGAG
 S G D E V Y S L A Y Y N Q P E
 1207 CAGGAATCAGTAGCAGCAGAAACCTGGGGACACATATGGAGGAC
 Q E S V A A E T L G T H M E D
 1252 AAGGTTTCCTTAGACATCTATTCCAGGCTGAGGAAAGCAAACATT
 K V S L D I Y S R L R K A N I 330
 1297-ACAGATGTGGACTATGAAGATGCTATGTAA 1326 339
 T D V D Y E D A M *
 GGT ATGGAAGATT CTGCTCTTTG
 1351 AAAACCATCC ATGACCCCAA GCCTCAGGCC TGATATGTTT TTCAGAGATC
 1401 CTGGGGCATT AGCTTTCCAG TATACCTCTT CTGGATGCCA TTCTCCATGG
 1451 CACTATTCTT TCATCTACTG TGAAGTGAAG TTGGCGCAGC CCTGAAGAAA
 1501 CTACCTAGGA GAACATAAG ACACAGGAGT GACAGGGACT TTGTTATCAG
 1551 AACCAGATTCT CTGCCGGCTC CTTTGAACAC AGGTCATATT GTGCTCTTCT
 1601 GTTTACAAGA GGAAACAAGA TGAATAAAA GAAATTGGGA TCCTGGGGTG
 1651 GAGGGACAGT GAAGCTTAGA GCACATGAAC TCAAGGTTAG TGACTCTGCA
 1701 GGACTTCACA GAGAGAGCTG TGCCCATCAT TCAGTCCAAG TGCTTTCTCT
 1751 GCCCAGACAG CACAGAACTC CAGCCCCGCT ACTTACATGG ATCATCGAGT
 1801 TTCCACCTAA AATATGATT TATTTATTT GAGTCACTGT TACCAAATTA

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[illegible]